

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:30:35 ; Search time 306.095 Seconds  
(without alignments)  
455.077 Million cell updates/sec

Title: US-10-712-882A-10

Perfect score: 20

Sequence: 1 ttcatatgaccccttcacg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 10399348

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	9	US-09-845-129-13
2	20	100.0	20	10	US-09-888-056A-6
3	20	100.0	20	15	US-10-167-127-30
4	20	100.0	20	16	US-10-172-919-14
5	20	100.0	20	19	US-10-802-061-13
6	20	100.0	20	20	US-10-823-197-14
7	20	100.0	20	21	US-10-712-882-8
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1	20	100.0	20	9	US-09-845-129-13
2	20	100.0	20	10	US-09-888-056A-6
3	20	100.0	20	15	US-10-167-127-30
4	20	100.0	20	16	US-10-172-919-14
5	20	100.0	20	19	US-10-802-061-13
6	20	100.0	20	20	US-10-823-197-14
7	20	100.0	20	21	US-10-712-882-8

20	100.0	20	100.0	20	21	US-10-712-882-10	Sequence 10, Appl
20	100.0	20	100.0	20	21	US-10-838-503-16	Sequence 16, Appl
10	15.8	79.0	20	22	22	US-10-681-773-70006	Sequence 70006, A
11	15.4	77.0	25	21	21	US-10-719-900-806734	Sequence 806734, A
12	15.4	77.0	25	21	21	US-10-809-189-75506	Sequence 75506, A
13	15.2	76.0	25	21	21	US-10-719-900-191746	Sequence 191746, A
14	15.2	76.0	25	13	13	US-10-156-820-14	Sequence 14, Appl
15	14.8	74.0	25	21	21	US-10-719-900-42232	Sequence 42232, A
16	14.8	74.0	25	22	22	US-10-843-527-22073	Sequence 22073, A
17	14.8	74.0	25	22	22	US-10-843-527-214640	Sequence 214640, A
18	14.8	74.0	25	22	22	US-10-681-773-26899	Sequence 26899, A
19	14.8	74.0	25	22	22	US-10-681-773-86218	Sequence 86218, A
20	14.8	74.0	25	22	22	US-10-681-773-113411	Sequence 113411, A
21	14.8	74.0	25	22	22	US-10-681-773-118725	Sequence 118725, A
22	14.4	72.0	25	21	21	US-10-719-900-435685	Sequence 435685, A
23	14.4	72.0	25	21	21	US-10-809-189-75507	Sequence 75507, A
24	14.2	71.0	20	22	22	US-10-601-497B-117	Sequence 117, App
25	14.2	71.0	25	21	21	US-10-719-900-631380	Sequence 631380, A
26	14.2	71.0	25	22	22	US-10-681-773-70007	Sequence 70007, A
27	14.2	71.0	25	22	22	US-10-719-956-36681	Sequence 36681, A
28	14.2	71.0	25	24	24	US-11-036-317-905193	Sequence 905193, A
29	14.2	71.0	25	24	24	US-11-036-317-961899	Sequence 961899, A
30	14.2	71.0	33	9	9	US-09-394-137A-11	Sequence 11, Appl
31	14.2	71.0	33	9	9	US-09-976-718-11	Sequence 11, Appl
32	14.2	71.0	33	9	9	US-09-911-253-11	Sequence 11, Appl
33	14.2	71.0	33	16	16	US-10-322-138-54	Sequence 54, Appl
34	14.2	71.0	33	16	16	US-11-039-678A-11	Sequence 11, Appl
35	14.2	71.0	50	17	17	US-10-131-827-6580	Sequence 6580, Ap
36	14.2	71.0	50	17	17	US-10-131-827-6970	Sequence 6970, Ap
37	14	70.0	25	21	21	US-10-719-900-383404	Sequence 383404, A
38	14	70.0	25	22	22	US-10-681-773-24059	Sequence 24059, A
39	13.8	69.0	24	9	9	US-09-922-261-22	Sequence 22, Appl
40	13.8	69.0	25	21	21	US-10-427-696-114	Sequence 114, App
41	13.8	69.0	25	20	20	US-10-719-900-806733	Sequence 806733, A
42	13.8	69.0	25	21	21	US-10-956-157-268505	Sequence 268505, A
43	13.8	69.0	25	22	22	US-10-843-527-21095	Sequence 21095, A
44	13.8	69.0	25	22	22	US-10-843-527-73730	Sequence 73730, A
45	13.8	69.0	25	22	22	US-10-843-527-74700	Sequence 74700, A
46	13.8	69.0	25	22	22	US-10-843-527-162013	Sequence 162013, A
47	13.8	69.0	25	22	22	US-10-843-527-162983	Sequence 162983, A
48	13.8	69.0	25	22	22	US-10-843-527-215618	Sequence 215618, A
49	13.8	69.0	25	22	22	US-10-681-773-107752	Sequence 107752, A
50	13.8	69.0	25	24	24	US-11-036-317-651777	Sequence 651777, A
51	13.8	69.0	31	22	22	US-10-019-543B-11	Sequence 11, Appl
52	13.8	69.0	33	9	9	US-09-922-261-20	Sequence 20, Appl
53	13.8	69.0	45	9	9	US-09-922-261-18	Sequence 18, Appl
54	13.6	68.0	25	21	21	US-10-719-900-191745	Sequence 191745, A
55	13.6	68.0	25	21	21	US-10-719-900-239384	Sequence 239384, A
56	13.6	68.0	25	21	21	US-10-719-900-492351	Sequence 492351, A
57	13.6	68.0	25	21	21	US-10-719-900-498114	Sequence 498114, A
58	13.6	68.0	25	21	21	US-10-719-900-714080	Sequence 714080, A
59	13.6	68.0	25	22	22	US-10-681-773-60938	Sequence 60938, A
60	13.6	68.0	25	22	22	US-10-681-773-79968	Sequence 79968, A
61	13.6	68.0	25	22	22	US-10-681-773-84021	Sequence 84021, A
62	13.6	68.0	25	22	22	US-10-681-773-106329	Sequence 106329, A
63	13.6	68.0	25	22	22	US-10-719-956-6952	Sequence 6952, Ap
64	13.6	68.0	25	22	22	US-10-719-956-366027	Sequence 366027, A
65	13.6	68.0	25	22	22	US-10-719-956-659051	Sequence 659051, A
66	13.6	68.0	25	22	22	US-10-719-956-686874	Sequence 686874, A
67	13.4	67.0	25	21	21	US-10-719-900-183288	Sequence 183288, A
68	13.4	67.0	25	21	21	US-10-956-157-135731	Sequence 135731, A
69	13.4	67.0	25	24	24	US-11-036-317-131521	Sequence 131521, A
70	13.4	67.0	25	24	24	US-11-036-317-569748	Sequence 569748, A
71	13.4	67.0	25	24	24	US-11-036-317-569749	Sequence 569749, A
72	13.4	67.0	25	24	24	US-11-036-317-633009	Sequence 633009, A
73	13.4	67.0	25	20	20	US-09-873-873-19	Sequence 19, Appl
74	13.2	66.0	20	9	9	US-09-916-956A-19	Sequence 19, Appl
75	13.2	66.0	20	10	10	US-09-997-914-19	Sequence 19, Appl
76	13.2	66.0	20	16	16	US-10-365-645-19	Sequence 19, Appl
77	13.2	66.0	20	18	18	US-10-672-163-19	Sequence 19, Appl
78	13.2	66.0	20	19	19	US-10-733-482-19	Sequence 19, Appl
79	13.2	66.0	20	19	19	US-10-817-182-19	Sequence 19, Appl

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:11:51 ; Search time 49.0476 seconds  
(without alignments)  
667.220 Million cell updates/sec

Title: US-10-712-882A-10

Perfect score: 20

Sequence: 1 ttacatagagcctccatg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents NA: \*  
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3: /cgn2\_6/ptodata/1/ina/6A COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PTCUS COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	US-08-510-696-2
2	20	100.0	20	3	US-09-345-217-13
3	20	100.0	20	4	US-09-845-129-13
4	20	100.0	20	4	US-09-037-472-8
5	20	100.0	20	4	US-09-037-472-10
6	20	100.0	20	4	US-09-578-534-14
7	20	100.0	20	4	US-09-632-657-16
8	20	100.0	20	4	US-09-693-555A-2
9	20	100.0	20	4	US-09-693-555A-18
10	20	100.0	20	4	US-09-584-950-18
11	20	100.0	20	5	PCI-US96-12455-2
12	18.4	92.0	21	3	US-09-035-220-14
13	18.4	92.0	21	3	US-09-035-220-23
14	18.4	92.0	25	3	US-09-035-220-10
15	18.4	92.0	25	3	US-09-035-220-19
16	18.4	92.0	26	3	US-09-035-220-9
17	18.4	92.0	26	3	US-09-035-220-18
18	18.4	92.0	27	3	US-09-035-220-8
19	18.4	92.0	27	3	US-09-035-220-17
20	18.4	92.0	28	3	US-09-035-220-7
21	18.4	92.0	28	3	US-09-035-220-16
22	18.4	92.0	29	3	US-09-035-220-6
23	18.4	92.0	29	3	US-09-035-220-15
24	18	90.0	19	3	US-09-035-220-5
25	17.4	87.0	23	3	US-09-035-220-11
26	17.4	87.0	23	3	US-09-035-220-20
27	16.4	82.0	21	3	US-09-035-220-12
28	16.4	82.0	21	3	US-09-035-220-21
29	16.4	82.0	21	3	US-09-396-196G-75506
30	15.4	77.0	21	3	US-09-396-196G-75506
31	15.4	76.0	25	4	US-09-155-613A-14
32	14.4	72.0	18	3	US-09-035-220-13
33	14.4	72.0	18	3	US-09-035-220-22
34	14.4	72.0	20	3	US-09-517-467B-118
35	14.4	72.0	25	4	US-09-396-196G-75507
36	14.2	71.0	33	1	US-08-390-192-2
37	14.2	71.0	33	3	US-09-120-049-11
38	14.2	71.0	33	3	US-09-394-137A-11
39	14.2	71.0	33	3	US-09-632-113-11
40	13.8	69.0	21	4	US-09-120-049-11
41	13.8	69.0	24	3	US-09-657-472-989
42	13.8	69.0	33	3	US-09-461-697-20
43	13.8	69.0	45	3	US-09-461-697-18
44	13.2	66.0	20	3	US-08-754-490-19
45	13.2	66.0	20	3	US-08-922-505A-19
46	13.2	66.0	20	3	US-09-260-952A-19
47	13.2	66.0	20	3	US-09-253-341-19
48	13.2	66.0	20	3	US-09-253-331A-19
49	13.2	66.0	20	3	US-09-261-040-19
50	13.2	66.0	20	4	US-09-916-956A-19
51	13.2	66.0	20	4	US-09-873-873-19
52	13.2	66.0	20	4	US-09-997-914-19
53	13.2	66.0	20	4	US-09-636-746B-19
54	13.2	66.0	20	4	US-10-365-645-19
55	13	65.0	33	1	US-07-854-596B-32
56	12.8	64.0	25	4	US-09-396-196G-14310
57	12.6	63.0	24	2	US-08-103-408A-1
58	12.6	63.0	24	2	US-08-103-408A-2
59	12.6	63.0	25	4	US-09-396-196G-17955
60	12.6	63.0	25	4	US-09-396-196G-78519
61	12.6	63.0	26	2	US-08-876-546A-13
62	12.6	63.0	26	3	US-09-412-252-13
63	12.6	63.0	42	1	US-07-834-539A-35
64	12.6	63.0	42	2	US-08-800-353-35
65	12.6	63.0	42	5	PCT-US92-06185-35
66	12.4	62.0	25	4	US-09-396-196G-36409
67	12.4	62.0	25	4	US-09-396-196G-63410
68	12.4	62.0	25	4	US-09-396-196G-63743
69	12.4	62.0	25	4	US-09-396-196G-83252
70	12.4	62.0	33	3	US-08-630-172-22
71	12.4	62.0	33	3	US-09-375-419-22
72	12.4	62.0	47	4	US-09-422-978-202
73	12.4	62.0	47	4	US-09-422-978-243
74	12.4	62.0	47	4	US-09-422-978-1342
75	12.4	62.0	49	3	US-09-550-338-12
76	12.4	62.0	49	4	US-09-767-878-12
77	12.2	61.0	21	4	US-09-657-472-1795
78	12.2	61.0	23	2	US-08-506-864A-21
79	12.2	61.0	23	2	US-08-851-968-21
80	12.2	61.0	25	4	US-09-396-196G-78494
81	12.2	61.0	25	4	US-09-396-196G-86904
82	12.2	61.0	28	4	US-10-327-189-13
83	12.2	61.0	32	1	US-08-437-815-9
84	12.2	61.0	32	1	US-08-897-040-9
85	12.2	61.0	32	3	US-09-039-866-2
86	12.2	61.0	36	1	US-08-256-261-18
87	12.2	61.0	36	1	US-08-256-261-19
88	12.2	61.0	36	1	US-08-256-261-26
89	12.2	61.0	36	1	US-08-256-261-27
90	12.2	61.0	36	1	US-08-852-299-18
91	12.2	61.0	36	3	US-08-852-299-19
92	12.2	61.0	36	3	US-08-852-299-26
93	12.2	61.0	36	3	US-08-852-299-27
94	12.2	61.0	37	1	US-08-488-700-16
95	12.2	61.0	37	2	US-08-704-706A-16
96	12.2	61.0	37	3	US-08-985-659-16
97	12.2	61.0	41	3	US-08-390-874C-3
98	12.2	61.0	41	3	US-09-265-772-3
99	12.2	61.0	44	3	US-09-390-874C-5
100	12.2	61.0	44	3	US-09-265-772-5

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:46:26 ; Search time 1296.76 Seconds  
(without alignments)  
587.066 Million cell updates/sec

Title: US-10-712-882A-10

Perfect score: 20  
Sequence: 1 ttacatagccttcacatg 20

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database: EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hic:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gsa1:\*
- 9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.8	69.0	49	4	BM812518 rt01d07.y
2	13.4	67.0	42	9	AL736015 Danio rer
3	13.2	66.0	25	7	L32055 HUMXP664A H
4	13.2	66.0	37	8	AZ827794 2M0104L22
5	12.6	63.0	31	9	AJ587203 Arabidops
6	12.6	63.0	37	1	AA190063 mu53d09.r
7	12.6	63.0	40	9	CL528515 ASV18C05
8	12.6	63.0	44	9	BM62564 Arabidops
9	12.6	63.0	48	8	BM46502 SALK_0084
10	12.4	62.0	37	1	AA611583
11	12.4	62.0	44	8	AZ598581
12	12.4	62.0	47	8	AZ424611 1M0413P22
13	12.2	61.0	38	9	AL758940 Arabidops
14	12.2	61.0	44	9	AL758939 Arabidops
15	12.2	61.0	49	1	AI808123
16	12.2	61.0	49	7	CO732619
17	12.0	60.0	26	8	AZ478579
18	12.0	60.0	35	9	DR2811S
19	11.8	59.0	40	1	AI195081
20	11.8	59.0	37	8	BH789296
21	11.8	59.0	41	8	BZ766913
22	11.8	59.0	47	8	BH792501
23	11.8	59.0	50	8	BZ769278
24	11.8	59.0	50	9	BX285636 Arabidops

C 25	11.6	58.0	35	5	BP938543
C 26	11.6	58.0	38	9	AG197154
C 27	11.6	58.0	38	9	TA14H06Q
C 28	11.6	58.0	39	8	AZ989699
C 29	11.6	58.0	40	9	AG194303
C 30	11.6	58.0	43	1	AA633126
C 31	11.6	58.0	43	6	AD576986
C 32	11.6	58.0	44	8	BH901178
C 33	11.6	58.0	44	9	AL945796
C 34	11.6	58.0	46	1	AI941389
C 35	11.6	58.0	46	9	BX292065
C 36	11.6	58.0	47	9	BX948761
C 37	11.6	58.0	47	9	CR400108
C 38	11.4	57.0	23	8	CC458169
C 39	11.4	57.0	36	8	AZ343296
C 40	11.4	57.0	43	9	CL517777
C 41	11.4	57.0	44	9	AG188343
C 42	11.2	56.0	28	9	TA223804P
C 43	11.2	56.0	30	9	CL521134
C 44	11.2	56.0	32	8	BZ291860
C 45	11.2	56.0	33	9	AG237320
C 46	11.2	56.0	37	1	AI080423
C 47	11.2	56.0	38	8	AZ601135
C 48	11.2	56.0	43	1	AI789500
C 49	11.2	56.0	44	1	AV834093
C 50	11.2	56.0	46	8	BH863326
C 51	11.2	56.0	48	9	BX663236
C 52	11.2	56.0	50	8	AZ565607
C 53	11.2	56.0	50	8	BH790392
C 54	11.1	55.0	23	8	AZ361811
C 55	11.1	55.0	26	8	AZ441490
C 56	11.1	55.0	26	8	BH863464
C 57	11.1	55.0	31	9	AB082451
C 58	11.1	55.0	32	4	BJ031457
C 59	11.1	55.0	32	8	BZ767797
C 60	11.1	55.0	33	8	AZ389099
C 61	11.1	55.0	33	8	AZ428294
C 62	11.1	55.0	34	8	AZ810486
C 63	11.1	55.0	34	8	CC060061
C 64	11.1	55.0	37	8	BH811874
C 65	11.1	55.0	37	8	BZ356214
C 66	11.1	55.0	37	8	BZ356684
C 67	11.1	55.0	39	1	AU010542
C 68	11.1	55.0	39	8	BZ353245
C 69	11.1	55.0	42	9	TA116801P
C 70	11.1	55.0	43	1	AJ619968
C 71	11.1	55.0	43	1	AU014004
C 72	11.1	55.0	44	9	AG201342
C 73	11.1	55.0	45	8	AZ435105
C 74	11.1	55.0	47	8	AZ490009
C 75	11.1	55.0	47	8	BZ356253
C 76	11.1	55.0	47	9	CL212987
C 77	11.1	55.0	48	8	BH642302
C 78	11.1	55.0	48	8	BH907010
C 79	11.1	55.0	50	1	AF077755
C 80	11.1	55.0	50	8	BZ763610
C 81	10.8	54.0	26	9	TA30H08Q
C 82	10.8	54.0	28	8	AZ358524
C 83	10.8	54.0	29	8	AZ812552
C 84	10.8	54.0	31	7	U44252
C 85	10.8	54.0	31	9	BX653330
C 86	10.8	54.0	33	8	AZ818537
C 87	10.8	54.0	35	8	BZ593677
C 88	10.8	54.0	36	8	BZ379829
C 89	10.8	54.0	37	7	CF305573
C 90	10.8	54.0	37	8	BH853989
C 91	10.8	54.0	37	8	BH865481
C 92	10.8	54.0	39	8	AZ463705
C 93	10.8	54.0	39	8	AZ992897
C 94	10.8	54.0	39	8	BZ664670
C 95	10.8	54.0	40	8	BH864614
C 96	10.8	54.0	40	8	BZ355646
C 97	10.8	54.0	41	8	BH855201

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 16:54:30 ; Search time 173.048 Seconds  
(without alignments)  
684.175 Million cell updates/sec

Title: US-10-712-882A-10

Perfect score: 20

Sequence: 1 ttacatagagccttcctg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- N Geneseqn\_16Dec04:\*
- 1: Geneseqn1980s:\*
  - 2: Geneseqn1990s:\*
  - 3: Geneseqn2000s:\*
  - 4: Geneseqn2001s:\*
  - 5: Geneseqn2002as:\*
  - 6: Geneseqn2002bs:\*
  - 7: Geneseqn2003as:\*
  - 8: Geneseqn2003bs:\*
  - 9: Geneseqn2003cs:\*
  - 10: Geneseqn2003ds:\*
  - 11: Geneseqn2004as:\*
  - 12: Geneseqn2004bs:\*
  - 13: Geneseqn2004cs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	100.0	20	2	AAT13884 Primer fo
2	20	100.0	20	2	AAV32396 Interleuk
3	4	20	100.0	20	AAZ10701 PCR prime
4	20	100.0	20	2	AAZ10701 PCR prime
5	20	100.0	20	2	AAZ10701 PCR prime
6	20	100.0	20	2	AAZ10701 PCR prime
7	20	100.0	20	2	AAZ10701 PCR prime
8	20	100.0	20	2	AAZ10701 PCR prime
9	20	100.0	20	2	AAZ10701 PCR prime
10	20	100.0	20	2	AAZ10701 PCR prime
11	20	100.0	20	2	AAZ10701 PCR prime
12	20	100.0	20	2	AAZ10701 PCR prime
13	20	100.0	20	2	AAZ10701 PCR prime
14	20	100.0	20	2	AAZ10701 PCR prime
15	20	100.0	20	2	AAZ10701 PCR prime
16	20	100.0	20	2	AAZ10701 PCR prime
17	18.4	92.0	21	3	AAZ10701 PCR prime
18	18.4	92.0	21	3	AAZ10701 PCR prime
19	18.4	92.0	21	3	AAZ10701 PCR prime
20	18.4	92.0	21	3	AAZ10701 PCR prime

21	18.4	92.0	26	3	AAZ10701 PCR prime
22	18.4	92.0	26	3	AAZ10701 PCR prime
23	18.4	92.0	26	3	AAZ10701 PCR prime
24	18.4	92.0	26	3	AAZ10701 PCR prime
25	18.4	92.0	26	3	AAZ10701 PCR prime
26	18.4	92.0	26	3	AAZ10701 PCR prime
27	18.4	92.0	26	3	AAZ10701 PCR prime
28	18.4	92.0	26	3	AAZ10701 PCR prime
29	18.4	92.0	26	3	AAZ10701 PCR prime
30	18.4	92.0	26	3	AAZ10701 PCR prime
31	18.4	92.0	26	3	AAZ10701 PCR prime
32	18.4	92.0	26	3	AAZ10701 PCR prime
33	18.4	92.0	26	3	AAZ10701 PCR prime
34	18.4	92.0	26	3	AAZ10701 PCR prime
35	18.4	92.0	26	3	AAZ10701 PCR prime
36	18.4	92.0	26	3	AAZ10701 PCR prime
37	18.4	92.0	26	3	AAZ10701 PCR prime
38	18.4	92.0	26	3	AAZ10701 PCR prime
39	18.4	92.0	26	3	AAZ10701 PCR prime
40	18.4	92.0	26	3	AAZ10701 PCR prime
41	18.4	92.0	26	3	AAZ10701 PCR prime
42	18.4	92.0	26	3	AAZ10701 PCR prime
43	18.4	92.0	26	3	AAZ10701 PCR prime
44	18.4	92.0	26	3	AAZ10701 PCR prime
45	18.4	92.0	26	3	AAZ10701 PCR prime
46	18.4	92.0	26	3	AAZ10701 PCR prime
47	18.4	92.0	26	3	AAZ10701 PCR prime
48	18.4	92.0	26	3	AAZ10701 PCR prime
49	18.4	92.0	26	3	AAZ10701 PCR prime
50	18.4	92.0	26	3	AAZ10701 PCR prime
51	18.4	92.0	26	3	AAZ10701 PCR prime
52	18.4	92.0	26	3	AAZ10701 PCR prime
53	18.4	92.0	26	3	AAZ10701 PCR prime
54	18.4	92.0	26	3	AAZ10701 PCR prime
55	18.4	92.0	26	3	AAZ10701 PCR prime
56	18.4	92.0	26	3	AAZ10701 PCR prime
57	18.4	92.0	26	3	AAZ10701 PCR prime
58	18.4	92.0	26	3	AAZ10701 PCR prime
59	18.4	92.0	26	3	AAZ10701 PCR prime
60	18.4	92.0	26	3	AAZ10701 PCR prime
61	18.4	92.0	26	3	AAZ10701 PCR prime
62	18.4	92.0	26	3	AAZ10701 PCR prime
63	18.4	92.0	26	3	AAZ10701 PCR prime
64	18.4	92.0	26	3	AAZ10701 PCR prime
65	18.4	92.0	26	3	AAZ10701 PCR prime
66	18.4	92.0	26	3	AAZ10701 PCR prime
67	18.4	92.0	26	3	AAZ10701 PCR prime
68	18.4	92.0	26	3	AAZ10701 PCR prime
69	18.4	92.0	26	3	AAZ10701 PCR prime
70	18.4	92.0	26	3	AAZ10701 PCR prime
71	18.4	92.0	26	3	AAZ10701 PCR prime
72	18.4	92.0	26	3	AAZ10701 PCR prime
73	18.4	92.0	26	3	AAZ10701 PCR prime
74	18.4	92.0	26	3	AAZ10701 PCR prime
75	18.4	92.0	26	3	AAZ10701 PCR prime
76	18.4	92.0	26	3	AAZ10701 PCR prime
77	18.4	92.0	26	3	AAZ10701 PCR prime
78	18.4	92.0	26	3	AAZ10701 PCR prime
79	18.4	92.0	26	3	AAZ10701 PCR prime
80	18.4	92.0	26	3	AAZ10701 PCR prime
81	18.4	92.0	26	3	AAZ10701 PCR prime
82	18.4	92.0	26	3	AAZ10701 PCR prime
83	18.4	92.0	26	3	AAZ10701 PCR prime
84	18.4	92.0	26	3	AAZ10701 PCR prime
85	18.4	92.0	26	3	AAZ10701 PCR prime
86	18.4	92.0	26	3	AAZ10701 PCR prime
87	18.4	92.0	26	3	AAZ10701 PCR prime
88	18.4	92.0	26	3	AAZ10701 PCR prime
89	18.4	92.0	26	3	AAZ10701 PCR prime
90	18.4	92.0	26	3	AAZ10701 PCR prime
91	18.4	92.0	26	3	AAZ10701 PCR prime
92	18.4	92.0	26	3	AAZ10701 PCR prime
93	18.4	92.0	26	3	AAZ10701 PCR prime

AAC63009	Human IL-
AAC63018	Human IL-
AAC63008	Human IL-
AAC63017	Human IL-
AAC63016	Human IL-
AAC63007	Human IL-
AAC63006	Human IL-
AAC63015	Human IL-
AAC63005	Human IL-
AAC63011	Human IL-
AAC63020	Human IL-
AAC63012	Human IL-
AAC63021	Human IL-
AAV42902	PCR prime
ACC63555	Murine ol
ACC63022	Human IL-
AAC63013	Human IL-
AAC63017	Human PAR
AAC63013	Human PAR
Adf43826	HPV 39 de
AAT36179	Human imm
AAV20488	HIV-1 pro
Aaz90231	HIV-1 PCR
Aah19879	HIV-1 pro
ABL55798	Human imm
ABV72353	PCR prime
ABQ78483	PCR prime
ABZ06589	Human leu
ABZ06979	Human leu
AAV96224	Human gen
AAB84143	Human cel
ABA96431	PCR prime
AAB84142	Human cel
AAB84141	Human cel
AAC81310	Mouse apo
AAZ86699	Primer pH
Aaz59078	Primer P3
Ado1826	PCR prime
Ado1825	PCR prime
Aav31181	Bacillus
ABK11827	Exchange
ADJ35187	B. thurin
ADG91981	PEG1089 p
ADT04943	Cryptospor
ABZ80305	Mouse gp1
ADP03251	PCR prime
AAD13126	Human mem
AAO2560	Human ser
AAAD13158	Human mem
AAAD13146	Human MTS
ABZ45480	Human ATP
ABZ46886	Human ATP
ADZ5786	PCR prime
ADQ62057	Anti-CD2
ADP85829	Mitochond
ADZ34621	POSH prot
ADG34657	Y. 12/200
ADR55725	Drug ther
ADR55724	Drug ther
ADZ18669	Fluoresce
ADD36629	Human pap
ADD22207	HPV E6 ge
Aaz65855	Human map
Aaz65896	Human map
AAG02558	NDF prime
ADf44773	Artificia
ADG83994	Human pap
ADf43896	HPV 45 de
Aaf97030	Human gen
Aav08436	SNuPE pri
Aav08437	SNuPE pri
ACI51890	Human mlc
AAZ05243	HIV-1 con

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:41:56 ; Search time 694.476 Seconds  
(without alignments)  
1395.446 Million cell updates/sec

Title: US-10-712-882A-10

Perfect score: 20

Sequence: 1 ttacatagccttcctcatg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	6	A82468 Sequence 6
2	20	100.0	20	6	I73226 Sequence 2
3	20	100.0	20	6	AR487076 Sequence
4	20	100.0	20	6	AR490516 Sequence
5	20	100.0	20	6	AR490518 Sequence
6	20	100.0	20	6	AR493821 Sequence
7	20	100.0	20	6	AR532953 Sequence
8	20	100.0	20	6	AR534175 Sequence
9	20	100.0	20	6	AR534191 Sequence
10	20	100.0	20	6	AR542782 Sequence
11	20	100.0	20	6	AX012488 Sequence
12	20	100.0	20	6	AX052804 Sequence
13	20	100.0	20	6	AX067277 Sequence
14	20	100.0	20	6	AX360020 Sequence
15	20	100.0	20	6	BD085846 Methods o
16	20	100.0	20	6	BD124529 Predictio
17	18.4	92.0	21	6	AR112246 Sequence
18	18.4	92.0	21	6	AR112255 Sequence
19	18.4	92.0	25	6	AR112242 Sequence

20	18.4	92.0	25	6	AR112251 Sequence
21	18.4	92.0	26	6	AR112241 Sequence
22	18.4	92.0	26	6	AR112250 Sequence
23	18.4	92.0	27	6	AR112240 Sequence
24	18.4	92.0	27	6	AR112249 Sequence
25	18.4	92.0	28	6	AR112239 Sequence
26	18.4	92.0	28	6	AR112248 Sequence
27	18.4	92.0	29	6	AR112238 Sequence
28	18.4	92.0	29	6	AR112247 Sequence
29	18	90.0	19	6	AR112237 Sequence
30	17.4	87.0	23	6	AR112243 Sequence
31	17.4	87.0	23	6	AR112252 Sequence
32	16.4	82.0	21	6	AR112244 Sequence
33	16.4	82.0	21	6	AR112253 Sequence
34	15.2	76.0	36	6	A87795 Sequence 14
35	15.2	76.0	36	6	AR218620 Sequence
36	14.4	72.0	17	6	AX723115 Sequence
37	14.4	72.0	18	6	AR112245 Sequence
38	14.4	72.0	18	6	AR112254 Sequence
39	14.4	72.0	20	6	AR230858 Sequence
40	14.2	71.0	20	6	BD184204 Method an
41	14.2	71.0	20	6	AX742380 Sequence
42	14.2	71.0	33	6	AR138757 Sequence
43	14.2	71.0	33	6	AR176895 Sequence
44	14.2	71.0	33	6	I34696 Sequence 2
45	14.2	71.0	33	6	AR183646 Sequence
46	14.2	71.0	33	6	AR262727 Sequence
47	14.2	71.0	33	6	AX003994 Sequence
48	13.8	69.0	21	6	AR529786 Sequence
49	13.8	69.0	21	6	AX095811 Sequence
50	13.8	69.0	31	6	BD103450 Transform
51	13.6	68.0	28	6	BD004102 Apoptosis
52	13.6	68.0	32	9	HUMTCVJ49
53	13.6	68.0	37	6	BD131641 Novel fun
54	13.2	66.0	20	6	AR107436 Sequence
55	13.2	66.0	20	6	AR156718 Sequence
56	13.2	66.0	20	6	AR166484 Sequence
57	13.2	66.0	20	6	AR179214 Sequence
58	13.2	66.0	20	6	AR282374 Sequence
59	13.2	66.0	20	6	AR301094 Sequence
60	13.2	66.0	20	6	AR429473 Sequence
61	13.2	66.0	20	6	AR490154 Sequence
62	13.2	66.0	20	6	AR544708 Sequence
63	13.2	66.0	20	6	AX383791 Sequence
64	13.2	66.0	20	6	BD007660 Delta-end
65	13.2	66.0	30	6	AX207916 Sequence
66	13.2	66.0	32	6	AX207944 Sequence
67	13.2	66.0	34	6	AX207936 Sequence
68	13.2	66.0	34	6	AX207949 Sequence
69	13.2	66.0	40	6	AX516066 Sequence
70	13.2	66.0	40	6	AX517472 Sequence
71	13	65.0	33	6	A20019
72	13	65.0	33	6	I13207
73	12.8	64.0	25	6	CQ864442 Sequence
74	12.8	64.0	25	6	CQ864443 Sequence
75	12.8	64.0	39	6	AX802743 Sequence
76	12.8	64.0	39	6	AX803126 Sequence
77	12.6	63.0	19	6	A15088
78	12.6	63.0	20	6	BD184274 Method an
79	12.6	63.0	20	6	AX742421 Sequence
80	12.6	63.0	24	6	AR063485 Sequence
81	12.6	63.0	24	6	AR063486 Sequence
82	12.6	63.0	25	6	AX610852 Sequence
83	12.6	63.0	26	6	AR078485 Sequence
84	12.6	63.0	26	6	AR152155 Sequence
85	12.6	63.0	35	6	AX938747 Sequence
86	12.6	63.0	38	6	AX933499 Sequence
87	12.6	63.0	38	6	AX933500 Sequence
88	12.6	63.0	42	6	I43946 Sequence 35
89	12.6	63.0	42	6	AX766986 Sequence
90	12.4	62.0	32	9	HUMTCVJ49
91	12.4	62.0	47	6	AR288467 Sequence
92	12.4	62.0	47	6	AR288508 Sequence

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:30:35 ; Search time 413.229 Seconds  
(without alignment)  
455.077 Million cell updates/sec

Title: US-10-712-882A-9  
Perfect score: 27  
Sequence: 1 aagctgtctaccacctaagcgc 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 10399348

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications NA:  
1: /cgm2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgm2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgm2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgm2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgm2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgm2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgm2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgm2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgm2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgm2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgm2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgm2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgm2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgm2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgm2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgm2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgm2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgm2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgm2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*  
20: /cgm2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cgm2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgm2\_6/ptodata/1/pubpna/US10J\_NEW\_PUB.seq.\*  
23: /cgm2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*  
24: /cgm2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgm2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgm2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	27	100.0	27 10	US-09-888-056A-5 Sequence 5, Appli
2	27	100.0	27 15	US-10-167-127-29 Sequence 29, Appli
3	27	100.0	27 16	US-10-172-919-13 Sequence 13, Appli
4	27	100.0	27 20	US-10-823-197-13 Sequence 13, Appli
5	27	100.0	27 21	US-10-712-882-1 Sequence 1, Appli
6	27	100.0	27 21	US-10-712-882-9 Sequence 9, Appli
7	27	100.0	27 21	US-10-838-503-15 Sequence 15, Appli

81.5	22	21	21	US-10-712-882-7	Sequence 7, Appli
77.8	21	9	9	US-09-845-129-12	Sequence 12, Appli
77.8	21	19	19	US-10-802-061-12	Sequence 12, Appli
62.2	25	15	15	US-10-098-263B-118759	Sequence 118759,
61.5	25	21	21	US-10-719-900-877295	Sequence 877295,
60.7	47	17	17	US-10-349-143-2940	Sequence 2940, Ap
60.0	25	22	22	US-10-681-773-8751	Sequence 8751, Ap
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59.3	25	21	21	US-10-719-900-500286	Sequence 500286,
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58.5	25	22	22	US-10-719-956-295391	Sequence 295391,
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57.8	25	21	21	US-10-719-900-441269	Sequence 441269,
57.8	25	21	21	US-10-809-189-103158	Sequence 103158,
57.8	25	22	22	US-10-719-956-641859	Sequence 641859,
57.8	25	24	24	US-11-036-317-88524	Sequence 88524, A
57.0	25	22	22	US-10-719-956-244717	Sequence 244717,
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56.3	25	22	22	US-10-719-956-47397	Sequence 47397, A
56.3	25	22	22	US-10-719-956-352728	Sequence 352728,
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55.6	25	21	21	US-10-956-157-64011	Sequence 64011, A
55.6	25	22	22	US-10-681-773-36476	Sequence 36476, A
55.6	25	22	22	US-10-681-773-119383	Sequence 119383,
54.8	25	21	21	US-10-719-900-844455	Sequence 844455,
54.8	25	21	21	US-10-956-157-250194	Sequence 250194,
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54.1	25	15	15	US-10-098-263B-78431	Sequence 78431, A
54.1	25	21	21	US-10-719-900-220387	Sequence 220387,
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54.1	25	21	21	US-10-719-900-770192	Sequence 770192,
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54.1	25	24	24	US-11-036-317-873765	Sequence 873765,
54.1	42	20	20	US-10-645-818-5	Sequence 5, Appli
53.3	25	21	21	US-10-719-900-112469	Sequence 112469,
53.3	25	21	21	US-10-719-900-150094	Sequence 150094,
53.3	25	21	21	US-10-719-900-163809	Sequence 163809,
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53.3	25	21	21	US-10-719-900-258835	Sequence 258835,
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53.3	25	21	21	US-10-719-900-425790	Sequence 425790,
53.3	25	21	21	US-10-719-900-500287	Sequence 500287,
53.3	25	21	21	US-10-719-900-602383	Sequence 602383,

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:11:51 ; Search time 66.2143 Seconds  
(Without alignments)  
667.220 Million cell updates/sec

Title: US-10-712-882A-9

Perfect score: 27

Sequence: 1 aagctgtttaccactgaactagggc 27

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PTCUS COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	3	US-09-035-220-4
2	27	100.0	27	4	US-09-037-472-1
3	27	100.0	27	4	US-09-037-472-9
4	27	100.0	27	4	US-09-578-534-13
5	27	100.0	27	4	US-09-632-657-15
6	27	100.0	27	4	US-09-693-555A-17
7	27	100.0	27	4	US-09-584-950-17
8	22	81.5	22	1	US-08-510-696-1
9	22	81.5	22	3	US-09-035-220-24
10	22	81.5	22	4	US-09-037-472-7
11	22	81.5	22	4	US-09-693-555A-1
12	22	81.5	22	5	PCT-US96-12455-1
13	21	77.8	21	3	US-09-345-217-12
14	21	77.8	21	4	US-09-845-129-12
15	16.4	60.7	47	4	US-09-422-978-2940
16	15.8	58.5	47	4	US-09-422-978-1413
17	15.6	57.8	25	4	US-09-396-196G-103158
18	15.6	57.8	39	1	US-08-231-342-18
19	14.8	54.8	20	1	US-07-661-591-2
20	14.4	53.3	44	6	5498600-32
21	14.4	53.3	44	6	5498600-32
22	14	51.9	25	4	US-09-396-196G-114726
23	13.8	51.1	19	1	US-08-832-883-29
24	13.8	51.1	19	2	US-08-832-877-29
25	13.8	51.1	25	4	US-09-396-196G-15819
26	13.8	51.1	25	4	US-09-396-196G-15820
27	13.8	51.1	25	4	US-09-396-196G-91950
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					Sequence 1, Appli
					Sequence 9, Appli
					Sequence 13, Appli
					Sequence 15, Appli
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					Sequence 17, Appli
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					Sequence 24, Appli
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					Sequence 12, Appli
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					Sequence 1413, Ap
					Sequence 103158,
					Sequence 18, Appli
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					Patent No. 5498600
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					Sequence 114726,
					Sequence 29, Appli
					Sequence 28, Appli
					Sequence 15819, A
					Sequence 15820, A
					Sequence 91950, A

28	13.8	51.1	31	1	US-08-361-337-45	Sequence 45, Appli
29	13.8	51.1	31	1	US-08-361-337-47	Sequence 47, Appli
c 30	13.6	50.4	25	4	US-09-396-196G-32442	Sequence 32442, A
31	13.6	50.4	25	4	US-09-396-196G-42568	Sequence 42568, A
c 32	13.6	50.4	25	4	US-09-396-196G-75782	Sequence 75782, A
c 33	13.4	49.6	23	1	US-08-227-689-4	Sequence 4, Appli
c 34	13.4	49.6	23	3	US-08-368-169-4	Sequence 4, Appli
35	13.4	49.6	25	4	US-09-396-196G-47479	Sequence 47479, A
36	13.4	49.6	25	4	US-09-396-196G-79756	Sequence 79756, A
37	13.4	49.6	28	3	US-08-936-632B-14	Sequence 14, Appli
c 38	13.4	49.6	29	4	US-09-769-863-7	Sequence 7, Appli
39	13.4	49.6	31	1	US-08-434-411-43	Sequence 43, Appli
40	13.4	49.6	31	1	US-08-434-402-43	Sequence 43, Appli
41	13.4	49.6	31	1	US-08-783-288-43	Sequence 43, Appli
42	13.4	49.6	31	2	US-08-890-640-43	Sequence 43, Appli
43	13.4	49.6	31	6	5194592-18	Patent No. 5194592
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c 45	13.4	49.6	33	1	US-08-434-411-44	Sequence 44, Appli
c 46	13.4	49.6	33	1	US-08-434-402-44	Sequence 44, Appli
c 47	13.4	49.6	33	1	US-08-783-288-44	Sequence 44, Appli
c 48	13.4	49.6	33	2	US-08-890-640-44	Sequence 44, Appli
c 49	13.2	48.9	19	4	US-09-043-944-15	Sequence 15, Appli
50	13.2	48.9	25	4	US-09-396-196G-37909	Sequence 37909, A
51	13.2	48.9	25	4	US-09-396-196G-42597	Sequence 42597, A
52	13.2	48.9	25	4	US-09-396-196G-91951	Sequence 91951, A
53	13.2	48.9	25	4	US-09-396-196G-91952	Sequence 91952, A
54	13.2	48.9	25	4	US-09-396-196G-116567	Sequence 116567, A
55	13.2	48.9	27	3	US-08-989-299-13	Sequence 13, Appli
56	13.2	48.9	27	4	US-09-407-427-13	Sequence 13, Appli
57	13.2	48.9	49	2	US-08-818-604-15	Sequence 15, Appli
58	13.2	48.9	49	4	US-09-346-946-15	Sequence 15, Appli
c 59	13	48.1	23	2	US-08-531-070A-15	Sequence 15, Appli
c 60	13	48.1	25	4	US-09-396-196G-23713	Sequence 23713, A
c 61	13	48.1	33	4	US-10-237-551-99	Sequence 99, Appli
c 62	13	48.1	33	4	US-10-237-551-101	Sequence 101, App
63	12.8	47.4	25	4	US-09-396-196G-2258	Sequence 2258, Ap
c 64	12.8	47.4	25	4	US-09-396-196G-8368	Sequence 8368, Ap
c 65	12.8	47.4	25	4	US-09-396-196G-8368	Sequence 8368, Ap
c 66	12.8	47.4	25	4	US-09-396-196G-9557	Sequence 9557, A
67	12.8	47.4	25	4	US-09-396-196G-32409	Sequence 32409, A
c 68	12.8	47.4	25	4	US-09-396-196G-41376	Sequence 41376, A
69	12.8	47.4	25	4	US-09-396-196G-47533	Sequence 47533, A
70	12.8	47.4	25	4	US-09-396-196G-72512	Sequence 72512, A
71	12.8	47.4	25	4	US-09-396-196G-72659	Sequence 72659, A
c 72	12.8	47.4	25	4	US-09-396-196G-91180	Sequence 91180, A
c 73	12.8	47.4	27	3	US-09-195-106-18	Sequence 18, Appli
c 74	12.8	47.4	29	1	US-08-246-982A-13	Sequence 13, Appli
c 75	12.8	47.4	29	1	US-08-453-265-13	Sequence 13, Appli
c 76	12.8	47.4	33	4	US-09-481-620A-126	Sequence 126, App
c 77	12.8	47.4	34	3	US-08-961-083-321	Sequence 321, App
c 78	12.8	47.4	34	4	US-09-536-784-321	Sequence 321, App
79	12.8	47.4	36	3	US-08-392-459-10	Sequence 10, Appli
80	12.8	47.4	36	4	US-09-854-799-10	Sequence 10, Appli
81	12.8	47.4	36	5	PCT-US91-08525-10	Sequence 10, Appli
82	12.8	47.4	36	5	PCT-US93-0438A-34	Sequence 34, Appli
c 83	12.8	47.4	38	3	US-08-961-083-239	Sequence 239, App
c 84	12.8	47.4	38	4	US-09-536-784-239	Sequence 239, App
85	12.8	47.4	50	4	US-08-443-613A-4	Sequence 4, Appli
86	12.8	47.4	50	5	PCT-US94-14889-4	Sequence 4, Appli
87	12.6	46.7	20	2	US-09-038-227-25	Sequence 25, Appli
88	12.6	46.7	21	3	US-08-928-213B-64	Sequence 64, Appli
89	12.6	46.7	21	4	US-09-657-472-1169	Sequence 1169, Ap
90	12.6	46.7	23	1	US-08-485-618-72	Sequence 72, Appli
91	12.6	46.7	23	1	US-08-362-652-72	Sequence 72, Appli
92	12.6	46.7	23	1	US-08-605-672-72	Sequence 72, Appli
93	12.6	46.7	23	2	US-08-482-293A-72	Sequence 72, Appli
94	12.6	46.7	23	2	US-08-943-363-72	Sequence 72, Appli
95	12.6	46.7	23	3	US-09-193-043-72	Sequence 72, Appli
96	12.6	46.7	23	3	US-09-688-307A-72	Sequence 72, Appli
97	12.6	46.7	23	4	US-09-350-259-72	Sequence 72, Appli
c 98	12.6	46.7	23	4	US-09-359-026C-10	Sequence 10, Appli
99	12.6	46.7	25	4	US-09-866-108A-5594	Sequence 5594, Ap
100	12.6	46.7	25	4	US-09-866-108A-5595	Sequence 5595, Ap

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:46:26 ; Search time 1750.63 Seconds  
(without alignments)  
587.066 Million cell updates/sec

Title: US-10-712-882A-9  
Perfect score: 27  
Sequence: 1 aagcttggtaccactgaactagc 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hlc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsl1:\*  
9: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 2	14	51.9	38	7	R82106 13D6 Chromo
C 3	13.8	51.1	50	7	CR437050 CR437050
C 4	13.4	49.6	42	1	AV833522 AV833522
C 5	13.4	49.6	43	1	AA445326 v55h02.r
C 6	13.2	48.9	36	9	BX892503 Arabidops
C 7	13.2	48.9	45	9	AL492651 T. brucei
C 8	12.8	47.4	32	8	AZ499485 LM0337113
C 9	12.8	47.4	37	9	AJ304156 Plasmid
C 10	12.8	47.4	44	4	BJ065975 BJ065975
C 11	12.8	47.4	50	8	AZ666536 IM0548D16
C 12	12.8	47.4	50	8	BH852799 SALK_0756
C 13	12.6	46.7	40	1	AA911795 ok74C09.s
C 14	12.6	46.7	43	1	AA121339 zn77d05.s
C 15	12.6	46.7	44	8	BZ770906 SALK_1439
C 16	12.6	46.7	46	9	CG800366 1118011A0
C 17	12.6	46.7	50	8	CC182113 02S2013-0
C 18	12.6	46.7	50	9	CR177236 Forward s
C 19	12.6	46.7	50	9	CG400426 01S0630-0
C 20	12.6	46.7	50	9	CG400440 01S0630-0
C 21	12.6	46.7	50	9	CG427403 01S0749-0
C 22	12.6	46.7	50	9	CL234330 02S0422-0
C 23	12.4	45.9	26	8	AZ779432 2M0015P14
C 24	12.4	45.9	27	8	BZ766391 SALK_1373

AZ396226	1M0160N09	30	8	AZ396226	45.9	12.4	25
AZ504924	1M0345B23	34	8	AZ504924	45.9	12.4	26
AZ627990	1M0476A08	35	8	AZ627990	45.9	12.4	C 27
CG783331	AST-2T009	37	8	AZ576414	45.9	12.4	C 28
CG783331	01S0530-0	38	9	CG783331	45.9	12.4	C 29
U21495	U21495 Huma	40	9	U21495	45.9	12.4	30
BX660493	Arabidops	43	9	BX660493	45.9	12.4	31
AU254169	AU254169	44	1	AU254169	45.9	12.4	32
BQ585750	R011419-0	46	5	BQ585750	45.9	12.4	C 33
CC458729	SALK_1217	48	8	CC458729	45.9	12.4	C 34
AI583675	tt74H06.x	31	1	AI583675	45.2	12.2	35
AZ474111	1M0290F22	33	8	AZ474111	45.2	12.2	C 36
AZ411075	1M0184B06	40	8	AZ411075	45.2	12.2	C 37
BZ380513	SALK_1152	44	8	BZ380513	45.2	12.2	C 38
AI636188	tz06E08.x	46	1	AI636188	45.2	12.2	C 39
AZ783979	2M0026K08	49	8	AZ783979	45.2	12.2	C 40
AJ593815	Arabidops	49	9	AJ593815	45.2	12.2	41
AU103054	AU103054	50	1	AU103054	45.2	12.2	C 42
CN973588	2109260-	50	7	CN973588	45.2	12.2	C 43
CO730398	SnESTbaa2	50	7	CO730398	45.2	12.2	C 44
CR203941	Forward s	50	9	CR203941	45.2	12.2	C 45
AZ434231	1M0220H03	30	8	AZ434231	44.4	12	46
BZ595231	SALK_0863	33	8	BZ595231	44.4	12	47
AA869975	vq10a06.r	34	1	AA869975	44.4	12	C 48
AI174397	an41c09.s	37	1	AI174397	44.4	12	C 49
AQ025245	EP(3)3062	38	1	AQ025245	44.4	12	50
AI282047	QG8F07.x	43	1	AI282047	44.4	12	51
BH906956	SALK_0368	43	8	BH906956	44.4	12	C 52
AA116551	md27F03.r	49	1	AA116551	44.4	12	C 53
AI176269	w156d08.x	49	1	AI176269	44.4	12	54
AV968446	AV968446	50	2	AV968446	44.4	12	55
CC516471	CH240_362	50	9	CC516471	44.4	12	56
AZ827644	2M0104N08	30	8	AZ827644	43.7	11.8	57
CG717990	1119051B1	31	9	CG717990	43.7	11.8	C 58
AZ812736	2M0079E09	32	8	AZ812736	43.7	11.8	C 59
AZ615836	1M0445D21	37	8	AZ615836	43.7	11.8	60
CC053460	SALK_0435	40	1	AA452048	43.7	11.8	C 62
AA452048	zx12F05.r	41	8	BH641362	43.7	11.8	C 63
BH641362	1008047A0	42	4	BG962762	43.7	11.8	C 64
BG962762	602830285	43	9	BX184327	43.7	11.8	C 65
BX184327	Danlo rer	44	8	BZ356371	43.7	11.8	66
AZ480534	1M0302E07	45	8	AZ480534	43.7	11.8	67
AZ769358	1M0569M20	45	8	AZ769358	43.7	11.8	C 68
BZ763663	SALK_1201	47	8	BZ763663	43.7	11.8	69
AV965281	AV965281	49	2	AV965281	43.7	11.8	C 70
AU104852	AU104852	50	1	AU104852	43.7	11.8	C 71
AU104853	AU104853	50	1	AU104853	43.7	11.8	C 72
AU104855	AU104855	50	1	AU104855	43.7	11.8	C 73
BG408716	gb77F07.y	50	4	BG408716	43.7	11.8	74
AZ635616	1M0493C18	50	8	AZ635616	43.7	11.8	75
CR129418	Reverse s	50	9	CR129418	43.7	11.8	C 76
AZ871751	2M0184I16	25	8	AZ871751	43.0	11.6	77
AZ619032	1M0451K07	34	8	AZ619032	43.0	11.6	78
BZ593763	SALK_0820	37	8	BZ593763	43.0	11.6	79
AA794942	vr05G03.r	45	1	AA794942	43.0	11.6	C 81
BX948798	Arabidops	45	9	BX948798	43.0	11.6	C 82
CG846879	01S0536-0	45	9	CG846879	43.0	11.6	C 83
BJ039761	BJ039761	46	1	BJ039761	43.0	11.6	84
AU243906	AU243906	48	1	AU243906	43.0	11.6	C 85
CD746731	S2Q3_B06	48	6	CD746731	43.0	11.6	C 86
AA673527	vn36F10.r	49	1	AA673527	43.0	11.6	87
AZ773638	2M0001010	49	8	AZ773638	43.0	11.6	C 88
BX178350	Danlo rer	49	9	BX178350	43.0	11.6	C 89
AU105749	AU105749	50	1	AU105749	43.0	11.6	C 90
AU107351	AU107351	50	1	AU107351	43.0	11.6	C 91
AU107686	AU107686	50	1	AU107686	43.0	11.6	C 92
AU107688	AU107688	50	1	AU107688	43.0	11.6	93
AZ921893	HRCoT3D04	50	8	AZ921893	43.0	11.6	94
AZ792320	2M0043N09	23	9	AG188248	42.2	11.4	95
AG188248	Pan trogl	29	8	BH848482	42.2	11.4	96
BH848482	SALK_0684	29	8	BZ381738	42.2	11.4	97



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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 16:54:30 ; Search time 233.614 Seconds  
(without alignments)  
684.175 Million cell updates/sec

Title: US-10-712-882A-9

Perfect score: 27  
Sequence: 1 agctgtgtctaccactgaactagc 27

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001as:\*
- 5: Geneseq2001bs:\*
- 6: Geneseq2002as:\*
- 7: Geneseq2002bs:\*
- 8: Geneseq2003as:\*
- 9: Geneseq2003bs:\*
- 10: Geneseq2003cs:\*
- 11: Geneseq2003ds:\*
- 12: Geneseq2004as:\*
- 13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	2	AAV32389 Interleuk
2	27	100.0	27	2	Aax10700 PC3 prime
3	27	100.0	27	2	Aax75921 Human int
4	27	100.0	27	3	Aax37218 PCR prime
5	27	100.0	27	3	Aac63004 Human IL-
6	27	100.0	27	5	Aac91431 Human IL-
7	27	100.0	27	5	Aad27381 PCR prime
8	27	100.0	27	8	Aal54507 Ageing-re
9	27	100.0	27	10	Aad51461 Human int
10	27	100.0	27	12	ADL8335 PCR prime
11	27	100.0	27	12	ADN48852 Human int
12	27	100.0	27	12	ADO35280 Human int
13	22	81.5	22	2	Aat70316 Primer fo
14	22	81.5	22	3	Aax37202 PCR prime
15	22	81.5	22	3	Aac63024 Human IL-
16	21	77.8	21	2	Aax16611 Interleuk
17	21	77.8	21	2	ABX15539 Human IL-
18	21	77.8	21	4	Aaf27676 Primer #9
19	16.8	62.2	25	9	ACK18778 Human mic
20	16.4	60.7	47	3	Aaz68591 Human map

C 21	15.8	58.5	47	3	AAZ67066	Aaz67066 Human map
C 22	15.2	56.3	25	9	ACK18779	ACK18779 Human mic
C 23	14.8	54.8	20	2	AAQ28501	AAQ28501 Polymeras
24	14.8	54.8	45	3	AAAS1868	AAAS1868 Primer fo
25	14.6	54.1	25	9	ACI78440	ACI78440 Human mic
26	14.6	54.1	25	9	ACI77838	ACI77838 Human mic
27	14.6	54.1	42	12	ADM36323	ADM36323 Bacteriopl
28	14.4	53.3	32	6	ABS52892	ABS52892 N-acetylgl
C 29	14.4	53.3	39	2	AAT61460	Aat61460 5' primer
C 30	14.2	52.6	19	2	AAV32395	AAV32395 Interleuk
C 31	14.2	52.6	25	9	ACI87658	ACI87658 Human mic
C 32	14.2	52.6	30	3	AAA73108	AAA73108 Human MCI
C 33	14.2	52.6	31	13	ADR73576	ADR73576 Staphyloc
C 34	14.2	52.6	35	4	AAL20650	Aal20650 Salmonell
C 35	14.2	52.6	35	9	AAL56578	Aal56578 PCR prime
C 36	14.2	52.6	38	4	AAF76985	Aaf76985 Human G p
C 37	14.2	52.6	41	4	AAL66442	Aal66442 DBH and p
C 38	14.2	52.6	41	12	ADK17885	Adk17885 Cytochrom
C 39	14.2	52.6	50	4	AAL32458	Aal32458 Human SNP
C 40	14.2	52.6	25	9	ACH56236	Ach56236 DNA targe
C 41	14.2	51.9	33	6	ABV75444	Abv75444 Human tra
C 42	14.2	51.9	41	6	ABZ44028	Abz44028 Human NDU
C 43	14.2	51.9	42	3	AAA29543	AAA29543 Codon alt
C 44	14.2	51.9	45	3	AAC58474	Aac58474 Human PRO
C 45	14.2	51.9	19	2	AAT96922	Aat96922 Human prb
C 46	13.8	51.1	25	9	ACK20090	Ack20090 Human mic
C 47	13.8	51.1	25	9	ACI57422	ACI57422 Human mic
C 48	13.8	51.1	25	9	ACI95662	ACI95662 Human mic
C 49	13.8	51.1	25	9	ACI95663	ACI95663 Human mic
C 50	13.8	51.1	25	9	ACK03316	Ack03316 Human mic
C 51	13.8	51.1	25	9	ACK02690	Ack02690 Human mic
C 52	13.8	51.1	25	9	ACK20726	Ack20726 Human mic
C 53	13.8	51.1	28	12	ADQ14756	Adq14756 N1a-speci
C 54	13.8	51.1	28	12	AAQ66552	Aaq66552 PCR prime
C 55	13.8	51.1	29	12	ADH23241	Adh23241 Stenotrosp
C 56	13.8	51.1	31	3	AAA79198	Aaa79198 Human gen
C 57	13.8	51.1	41	5	AAF62022	Aaf62022 Canine IL
C 58	13.8	51.1	41	11	ADP71353	Adp71353 Primer #1
C 59	13.8	51.1	41	11	ADP71354	Adp71354 Primer #2
C 60	13.8	51.1	48	13	ADQ89999	Adq89999 Primer of
C 61	13.8	51.1	50	4	AAL34269	Aal34269 Human SNP
C 62	13.8	51.1	50	12	ADP93983	Adp93983 Microorga
C 63	13.8	51.1	50	12	ADP94012	Adp94012 Microorga
C 64	13.8	51.1	50	12	ADP94015	Adp94015 Microorga
C 65	13.8	51.1	50	12	ADP94015	Adp94015 Microorga
C 66	13.6	50.4	20	6	AAJ72107	Aaj72107 pGL-VPR f
C 67	13.6	50.4	23	12	ADJ57664	Adj57664 Primer of
C 68	13.6	50.4	25	3	AAA92094	Aaa92094 Human Lhx
C 69	13.6	50.4	25	3	AAA92093	Aaa92093 Human Lhx
C 70	13.6	50.4	33	6	ABL54229	AbL54229 Human G-p
C 71	13.6	50.4	43	12	ADP97095	Adp97095 C. albica
C 72	13.6	50.4	46	10	ADP94287	Adp94287 Mouse HUI
C 73	13.6	50.4	50	6	ABZ07241	Abz07241 Human leu
C 74	13.4	49.6	21	10	ADD14293	Add14293 Human src
C 75	13.4	49.6	21	12	ADM10351	Adm10351 Human CYP
C 76	13.4	49.6	23	12	ADO25213	Ado25213 E. coli g
C 77	13.4	49.6	24	6	ABZ31657	Abz31657 Candida a
C 78	13.4	49.6	25	9	ACI63490	ACI63490 Human mic
C 79	13.4	49.6	25	9	ACI97672	ACI97672 Human mic
C 80	13.4	49.6	25	10	ADJ87874	Adj87874 G-coupled
C 81	13.4	49.6	25	12	ADO56055	Ado56055 Human NOV
C 82	13.4	49.6	28	2	AAV26909	Aav26909 PHO3 gene
C 83	13.4	49.6	28	4	AAF27377	Aaf27377 yeast Pho
C 84	13.4	49.6	29	8	ADA49058	Aad49058 Saprolegn
C 85	13.4	49.6	29	12	ADK60325	Adk60325 Angiogene
C 86	13.4	49.6	29	12	ADK60626	Adk60626 Angiogene
C 87	13.4	49.6	29	12	ADP73249	Adp73249 Primer of
C 88	13.4	49.6	31	12	ADJ03839	Adj03839 PCR prime
C 89	13.4	49.6	32	8	AAL52203	Aal52203 Human ret
C 90	13.4	49.6	32	12	ADJ03845	Adj03845 PCR prime
C 91	13.4	49.6	32	12	ADJ03841	Adj03841 PCR prime
C 92	13.4	49.6	32	12	ADJ03843	Adj03843 PCR prime
C 93	13.4	49.6	35	4	AAD20651	Aad20651 Salmonell

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:41:56 ; Search time 937.543 Seconds  
(without alignments)  
1395.446 Million cell updates/sec

Title: US-10-712-882A-9  
Perfect score: 27  
Sequence: 1 aagcttcttaccacgaactagc 27

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_ats.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	6	AR112236 Sequence
2	27	100.0	27	6	AR490509 Sequence
3	27	100.0	27	6	AR490517 Sequence
4	27	100.0	27	6	AR493820 Sequence
5	27	100.0	27	6	AR532952 Sequence
6	27	100.0	27	6	AR534190 Sequence
7	27	100.0	27	6	AR542781 Sequence
8	27	100.0	27	6	AX012487 Sequence
9	27	100.0	27	6	AX052803 Sequence
10	27	100.0	27	6	AX360019 Sequence
11	27	100.0	27	6	BD085845 Methods
12	22	81.5	22	6	AR112256 Sequence
13	22	81.5	22	6	I73225 Sequence 1
14	22	81.5	22	6	AR490515 Sequence
15	22	81.5	22	6	AR534174 Sequence
16	21	77.8	21	6	A82467 Sequence 5
17	21	77.8	21	6	AR487075 Sequence
18	21	77.8	21	6	AX067276 Sequence
19	21	77.8	21	6	BD124528 Predictio

45	6	AX027655	Sequence
47	6	AR291205	Sequence
47	6	AR289678	Sequence
39	6	AR050328	Sequence
20	6	I13552	Sequence 2
32	6	BD166382	DNA encod
39	6	E12937	PCR primer.
44	6	AR365487	Sequence
49	6	FCLTRNA	
28	6	CQ794117	Sequence
28	6	CQ800086	Sequence
30	6	E36185	Upstream re
35	6	AX254701	Sequence
35	6	AX766357	Sequence
38	6	BD012991	Novel G p
38	6	BD014502	Novel G p
50	6	CQ007026	Sequence
42	6	BD231118	Shuffling
42	10	AB002263	Mus muscu
19	6	AR038723	Sequence
19	6	AR059609	Sequence
31	6	I92393	Sequence 45
31	6	I92395	Sequence 47
31	6	BD002902	Gene comp
48	6	CQ848125	Sequence
50	6	CQ008837	Sequence
20	6	AX319716	Sequence
33	6	AX468847	Sequence
41	6	AX514614	Sequence
41	6	AX520556	Sequence
23	6	A22727	oligonucl
23	6	A47686	Sequence 4
23	6	I21369	Sequence 4
24	6	AX48576	Sequence
28	6	AR121174	Sequence
28	6	BD003589	Methods a
29	6	AR410189	Sequence
29	6	AX576982	Sequence
29	6	AX828555	Sequence
31	6	AR024399	Sequence
31	6	AR091772	Sequence
31	6	I71191	Sequence 43
31	6	I83750	Sequence 43
31	6	AR363050	Sequence
33	6	AR024400	Sequence
33	6	AR091773	Sequence
33	6	I71192	Sequence 44
33	6	I83751	Sequence 44
35	6	AX254702	Sequence
22	6	AX703202	Sequence
24	6	AX657568	Sequence
27	6	AR135179	Sequence
27	6	BD274686	Angiotens
27	6	AR382343	Sequence
27	6	AX418994	Sequence
28	6	CQ794114	Sequence
28	6	CQ800083	Sequence
29	6	BD140466	Secreted
30	6	BD143373	Oligonucl
33	6	BD179410	Screening
36	6	I03354	Sequence 4
42	6	AX060507	Sequence
42	6	AX317386	Sequence
42	6	AX317387	Sequence
45	6	AX283132	Sequence
49	6	AR075954	Sequence
49	6	AR322317	Sequence
23	6	AR067590	Sequence
26	6	BD143580	Method of
31	6	AX460476	Sequence
31	6	AX463680	Sequence
35	6	AX684693	Sequence
35	6	AX684695	Sequence

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:30:35 ; Search time 306.095 Seconds  
(without alignments)  
455.077 Million cell updates/sec

Title: US-10-712-882A-8

Perfect score: 20

Sequence: 1 ttcatatgaccccttcattg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 10399348

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA.\*  
1: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US10J\_PUBCOMB.seq.\*  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	20	100.0	20	US-09-845-129-13
2	20	100.0	20	US-09-888-056A-6
3	20	100.0	20	US-10-167-127-30
4	20	100.0	20	US-10-172-919-14
5	20	100.0	20	US-10-802-061-13
6	20	100.0	20	US-10-823-197-14
7	20	100.0	20	US-10-712-882-8
8	20	100.0	20	Sequence 13, Appl
9	20	100.0	20	Sequence 6, Appl
10	20	100.0	20	Sequence 30, Appl
11	20	100.0	20	Sequence 14, Appl
12	20	100.0	20	Sequence 13, Appl
13	20	100.0	20	Sequence 14, Appl
14	20	100.0	20	Sequence 8, Appl

Sequence 10, Appl	20	100.0	20	US-10-712-882-10
Sequence 16, Appl	20	100.0	20	US-10-838-503-16
Sequence 70006, A	25	15.8	79.0	US-10-681-773-70006
Sequence 806734, A	25	15.4	77.0	US-10-719-900-806734
Sequence 75506, A	25	15.4	77.0	US-10-809-189-75506
Sequence 191746, A	25	15.2	76.0	US-10-719-900-191746
Sequence 14, Appl	36	13.2	76.0	US-10-156-820-14
Sequence 42332, A	25	14.8	74.0	US-10-719-900-42332
Sequence 22073, A	25	14.8	74.0	US-10-843-527-22073
Sequence 214640, A	25	14.8	74.0	US-10-843-527-214640
Sequence 26899, A	25	14.8	74.0	US-10-681-773-26899
Sequence 86218, A	25	14.8	74.0	US-10-681-773-86218
Sequence 113411, A	25	14.8	74.0	US-10-681-773-113411
Sequence 118725, A	25	14.8	74.0	US-10-681-773-118725
Sequence 435685, A	25	14.4	72.0	US-10-719-900-435685
Sequence 75507, A	25	14.4	72.0	US-10-809-189-75507
Sequence 117, Appl	20	14.2	71.0	US-10-601-497B-117
Sequence 631380, A	25	14.2	71.0	US-10-719-900-631380
Sequence 70007, A	25	14.2	71.0	US-10-681-773-70007
Sequence 36681, A	25	14.2	71.0	US-10-719-956-36681
Sequence 905193, A	25	14.2	71.0	US-11-036-317-905193
Sequence 961899, A	25	14.2	71.0	US-11-036-317-961899
Sequence 11, Appl	33	14.2	71.0	US-09-394-137A-11
Sequence 11, Appl	33	14.2	71.0	US-09-976-718-11
Sequence 11, Appl	33	14.2	71.0	US-09-911-253-11
Sequence 54, Appl	33	14.2	71.0	US-10-322-138-54
Sequence 11, Appl	33	14.2	71.0	US-11-039-678A-11
Sequence 6580, Ap	50	14.2	71.0	US-10-131-827-6580
Sequence 6870, Ap	50	14.2	71.0	US-10-131-827-6870
Sequence 383404, A	25	14.0	70.0	US-10-719-900-383404
Sequence 24059, A	25	14.0	70.0	US-10-681-773-24059
Sequence 22, Appl	24	13.8	69.0	US-09-922-261-22
Sequence 114, App	25	13.8	69.0	US-10-427-696-114
Sequence 806733, A	25	13.8	69.0	US-10-719-900-806733
Sequence 268505, A	25	13.8	69.0	US-10-956-157-268505
Sequence 21095, A	25	13.8	69.0	US-10-843-527-21095
Sequence 73730, A	25	13.8	69.0	US-10-843-527-73730
Sequence 74700, A	25	13.8	69.0	US-10-843-527-74700
Sequence 162013, A	25	13.8	69.0	US-10-843-527-162013
Sequence 162983, A	25	13.8	69.0	US-10-843-527-162983
Sequence 215618, A	25	13.8	69.0	US-10-843-527-215618
Sequence 107752, A	25	13.8	69.0	US-10-681-773-107752
Sequence 651777, A	25	13.8	69.0	US-11-036-317-651777
Sequence 11, Appl	31	13.8	69.0	US-10-019-543B-11
Sequence 20, Appl	33	13.8	69.0	US-09-922-261-20
Sequence 18, Appl	45	13.6	68.0	US-09-922-261-18
Sequence 191745, A	25	13.6	68.0	US-10-719-900-191745
Sequence 219384, A	25	13.6	68.0	US-10-719-900-219384
Sequence 492351, A	25	13.6	68.0	US-10-719-900-492351
Sequence 498114, A	25	13.6	68.0	US-10-719-900-498114
Sequence 714080, A	25	13.6	68.0	US-10-719-900-714080
Sequence 60938, A	25	13.6	68.0	US-10-681-773-60938
Sequence 79968, A	25	13.6	68.0	US-10-681-773-79968
Sequence 84021, A	25	13.6	68.0	US-10-681-773-84021
Sequence 106329, A	25	13.6	68.0	US-10-681-773-106329
Sequence 6952, Ap	25	13.6	68.0	US-10-719-956-6952
Sequence 366027, A	25	13.6	68.0	US-10-719-956-366027
Sequence 659051, A	25	13.6	68.0	US-10-719-956-659051
Sequence 686874, A	25	13.6	68.0	US-10-719-956-686874
Sequence 183288, A	25	13.4	67.0	US-10-719-900-183288
Sequence 135731, A	25	13.4	67.0	US-10-956-157-135731
Sequence 226422, A	25	13.4	67.0	US-11-036-317-226422
Sequence 131521, A	25	13.4	67.0	US-11-036-317-131521
Sequence 569748, A	25	13.4	67.0	US-11-036-317-569748
Sequence 569749, A	25	13.4	67.0	US-11-036-317-569749
Sequence 613009, A	25	13.4	67.0	US-11-036-317-613009
Sequence 19, Appl	20	13.2	66.0	US-09-873-873-19
Sequence 19, Appl	20	13.2	66.0	US-09-916-956A-19
Sequence 19, Appl	20	13.2	66.0	US-09-997-914-19
Sequence 19, Appl	20	13.2	66.0	US-10-365-645-19
Sequence 19, Appl	20	13.2	66.0	US-10-672-163-19
Sequence 19, Appl	20	13.2	66.0	US-10-733-482-19
Sequence 19, Appl	20	13.2	66.0	US-10-817-182-19

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:11:51 ; Search time 49.0476 Seconds  
(without alignments)  
667.220 Million cell updates/sec

Title: US-10-712-882A-8

Perfect score: 20

Sequence: 1 ttacatagccttcacg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:\*

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- 2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*
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- 5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	US-08-510-696-2
2	20	100.0	20	3	US-09-345-217-13
3	20	100.0	20	4	US-09-845-129-13
4	20	100.0	20	4	US-09-037-472-8
5	20	100.0	20	4	US-09-037-472-10
6	20	100.0	20	4	US-09-578-534-14
7	20	100.0	20	4	US-09-632-657-16
8	20	100.0	20	4	US-09-693-555A-2
9	20	100.0	20	4	US-09-693-555A-18
10	20	100.0	20	4	US-09-584-950-18
11	20	100.0	20	5	PCT-US96-12455-2
12	18.4	92.0	20	3	US-09-035-220-14
13	18.4	92.0	20	3	US-09-035-220-23
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16	18.4	92.0	20	3	US-09-035-220-18
17	18.4	92.0	20	3	US-09-035-220-8
18	18.4	92.0	20	3	US-09-035-220-17
19	18.4	92.0	20	3	US-09-035-220-7
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21	18.4	92.0	20	3	US-09-035-220-6
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67	16.4	82.0	20	3	US-09-035-220-11
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69	16.4	82.0	20	3	US-09-035-220-9
70	16.4	82.0	20	3	US-09-035-220-8
71	16.4	82.0	20	3	US-09-035-220-7
72	16.4	82.0	20	3	US-09-035-220-6
73	16.4	82.0	20	3	US-09-035-220-5
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80	16.4	82.0	20	3	US-09-035-220-22
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82	16.4	82.0	20	3	US-09-035-220-14
83	16.4	82.0	20	3	US-09-035-220-18
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97	16.4	82.0	20	3	US-09-035-220-6
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22	3	US-09-396-196G-75506	Sequence 75506, A
23	4	US-09-155-613A-14	Sequence 14, Appl
24	3	US-09-035-220-13	Sequence 13, Appl
25	3	US-09-035-220-22	Sequence 22, Appl
26	3	US-09-517-467B-118	Sequence 118, App
27	4	US-09-396-196G-75507	Sequence 75507, A
28	1	US-08-390-192-2	Sequence 2, Appli
29	3	US-09-120-049-11	Sequence 11, Appl
30	3	US-09-394-137A-11	Sequence 11, Appl
31	3	US-09-632-113-11	Sequence 11, Appl
32	3	US-09-120-049-11	Sequence 11, Appl
33	4	US-09-657-472-989	Sequence 989, App
34	3	US-09-461-697-22	Sequence 22, Appl
35	3	US-09-461-697-20	Sequence 20, Appl
36	3	US-09-461-697-18	Sequence 18, Appl
37	3	US-08-754-490-19	Sequence 19, Appl
38	3	US-08-922-505A-19	Sequence 19, Appl
39	3	US-09-260-952A-19	Sequence 19, Appl
40	3	US-09-253-341-19	Sequence 19, Appl
41	3	US-09-253-331A-19	Sequence 19, Appl
42	3	US-09-261-040-19	Sequence 19, Appl
43	4	US-09-916-956A-19	Sequence 19, Appl
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47	4	US-10-365-645-19	Sequence 19, Appl
48	1	US-07-854-596B-32	Sequence 32, Appl
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50	4	US-08-103-408A-1	Sequence 1, Appli
51	2	US-08-103-408A-2	Sequence 2, Appli
52	4	US-09-396-196G-17955	Sequence 17955, A
53	4	US-09-396-196G-78519	Sequence 78519, A
54	2	US-08-876-546A-13	Sequence 13, Appl
55	3	US-09-412-252-13	Sequence 13, Appl
56	1	US-07-834-539A-35	Sequence 35, Appl
57	2	US-08-800-353-35	Sequence 35, Appl
58	4	PCT-US92-06185-35	Sequence 35, Appl
59	4	US-09-396-196G-36409	Sequence 36409, A
60	4	US-09-396-196G-36410	Sequence 36410, A
61	4	US-09-396-196G-63743	Sequence 63743, A
62	4	US-09-396-196G-83252	Sequence 83252, A
63	3	US-08-630-172-22	Sequence 22, Appl
64	3	US-09-375-419-22	Sequence 22, Appl
65	4	US-09-422-978-202	Sequence 202, App
66	4	US-09-422-978-243	Sequence 243, App
67	4	US-09-422-978-1342	Sequence 1342, Ap
68	3	US-09-550-338-12	Sequence 12, Appl
69	4	US-09-657-472-1795	Sequence 1795, Ap
70	2	US-08-506-864A-21	Sequence 21, Appl
71	2	US-08-851-968-21	Sequence 21, Appl
72	4	US-09-396-196G-78494	Sequence 78494, A
73	4	US-09-396-196G-86904	Sequence 86904, A
74	4	US-10-327-189-13	Sequence 13, Appl
75	3	US-08-437-815-9	Sequence 9, Appli
76	3	US-08-897-040-9	Sequence 9, Appli
77	3	US-09-039-866-2	Sequence 2, Appli
78	3	US-08-256-261-18	Sequence 18, Appl
79	3	US-08-256-261-19	Sequence 19, Appl
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81	3	US-08-256-261-27	Sequence 27, Appl
82	3	US-08-256-261-18	Sequence 18, Appl
83	3	US-08-852-299-19	Sequence 19, Appl
84	3	US-08-852-299-26	Sequence 26, Appl
85	3	US-08-852-299-22	Sequence 22, Appl
86	3	US-08-852-299-27	Sequence 27, Appl
87	3	US-08-468-700-16	Sequence 16, Appl
88	3	US-08-704-706A-16	Sequence 16, Appl
89	3	US-08-985-659-16	Sequence 16, Appl
90	4	US-08-390-874C-3	Sequence 3, Appli
91	4	US-09-265-772-3	Sequence 3, Appli
92	4	US-08-390-874C-5	Sequence 5, Appli
93	4	US-09-265-772-5	Sequence 5, Appli

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2	13.4	67.0	42	9	DR1L3S	AL736015 Danio rer
C 3	13.2	66.0	25	7	L32055	L32055 HUMXP664A.H
C 4	13.2	66.0	37	8	AZ827794	AZ827794 2M0104L22
5	12.6	63.0	31	9	AAJ587203	AAJ587203 Arabidops
C 6	12.6	63.0	37	1	AAJ90063	AAJ90063 mu53d09.r
C 7	12.6	63.0	40	9	CLS28515	CLS28515 ASV18C05.
8	12.6	63.0	49	9	BX662564	BX662564 Arabidops
C 9	12.6	63.0	48	8	BH946502	BH946502 SALK 0084
10	12.4	62.0	37	1	AA611583	AA611583 vo93b03.r
C 11	12.4	62.0	44	8	AZ598581	AZ598581 IM0413P22
C 12	12.4	62.0	47	8	AZ424611	AZ424611 IM0204K13
C 13	12.2	61.0	38	9	AL758940	AL758940 Arabidops
C 14	12.2	61.0	44	9	AL758939	AL758939 Arabidops
15	12.2	61.0	49	1	AI808123	AI808123 wf53d07.x
C 16	12.2	61.0	49	7	C0732619	C0732619 SL1501B02
17	12	60.0	26	8	AZ478579	AZ478579 IM0298E16
18	12	60.0	35	9	DR2811S	AL975868 Danio rer
C 19	12	60.0	40	1	AI195081	AI195081 ui60d06.x
C 20	11.8	59.0	37	8	BH789296	BH789296 SALK 0016
C 21	11.8	59.0	41	8	BZ768913	BZ768913 SALK 1413
C 22	11.8	59.0	47	8	BH792501	BH792501 SALK 0846
C 23	11.8	59.0	50	8	BZ769278	BZ769278 SALK 1419
C 24	11.8	59.0	50	9	BX285636	BX285636 Arabidops

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 16:54:30 ; Search time 173.048 Seconds  
(without alignments)  
684.175 Million cell updates/sec

Title: US-10-712-882A-8  
Perfect score: 20  
Sequence: 1 ttcatatgagccttcctg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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2: Geneseq\_1990s:.\*  
3: Geneseq\_2000s:.\*  
4: Geneseq\_2001as:.\*  
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6: Geneseq\_2002as:.\*  
7: Geneseq\_2002bs:.\*  
8: Geneseq\_2003as:.\*  
9: Geneseq\_2003bs:.\*  
10: Geneseq\_2003cs:.\*  
11: Geneseq\_2003ds:.\*  
12: Geneseq\_2004as:.\*  
13: Geneseq\_2004bs:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	AAT13884 Primer fo
2	20	100.0	20	2	AAV32396 Interleuk
3	20	100.0	20	2	AZ10701 PCR prime
4	20	100.0	20	2	AAX75922 Human int
5	20	100.0	20	2	AAX16612 Interleuk
6	20	100.0	20	2	ABX15540 Human IL-
7	20	100.0	20	3	AAX37219 PCR prime
8	20	100.0	20	3	AAX37203 PCR prime
9	20	100.0	20	4	AAX27677 Primer #1
10	20	100.0	20	5	AAC91432 Human IL-
11	20	100.0	20	6	AAD27382 PCR prime
12	20	100.0	20	8	AAL54508 Ageing-re
13	20	100.0	20	10	AAD51462 Human int
14	20	100.0	20	12	ADL83336 PCR prime
15	20	100.0	20	12	ADN48853 Human int
16	20	100.0	20	12	ADN48853 Human int
17	18.4	92.0	21	3	AAC63014 Human IL-
18	18.4	92.0	21	3	AAC63023 Human IL-
19	18.4	92.0	25	3	AAC63019 Human IL-
20	18.4	92.0	25	3	AAC63010 Human IL-

21	18.4	92.0	26	3	AAC63009 Human IL-
22	18.4	92.0	26	3	AAC63018 Human IL-
23	18.4	92.0	27	3	AAC63008 Human IL-
24	18.4	92.0	27	3	AAC63017 Human IL-
25	18.4	92.0	28	3	AAC63016 Human IL-
26	18.4	92.0	28	3	AAC63007 Human IL-
27	18.4	92.0	29	3	AAC63006 Human IL-
28	18.4	92.0	29	3	AAC63015 Human IL-
29	18	90.0	19	3	AAC63005 Human IL-
30	17.4	87.0	23	3	AAC63011 Human IL-
31	17.4	87.0	23	3	AAC63020 Human IL-
32	16.4	82.0	21	3	AAC63012 Human IL-
33	16.4	82.0	21	3	AAC63021 Human IL-
34	15.2	76.0	36	2	AAV42902 PCR prime
35	14.4	72.0	17	8	ACC63555 Murine ol
36	14.4	72.0	18	3	AAC63022 Human IL-
37	14.4	72.0	18	3	AAC63013 Human IL-
38	14.4	72.0	20	4	AAS45697 Human PAR
39	14.2	71.0	20	4	AAS45697 Human PAR
40	14.2	71.0	20	10	ADC83953 Human pap
41	14.2	71.0	20	10	ADF43826 HPV 39 de
42	14.2	71.0	33	2	AAT36179 Human imm
43	14.2	71.0	33	2	AAV20488 HIV-1 pro
44	14.2	71.0	33	3	AAZ90231 HIV-1 PCR
45	14.2	71.0	33	4	AAH19879 Human imm
46	14.2	71.0	33	6	ABL55798 Human imm
47	14.2	71.0	33	6	ABV72353 PCR prime
48	14.2	71.0	50	6	ABZ06589 Human leu
49	14.2	71.0	50	6	ABZ06589 Human leu
50	13.8	69.0	21	4	AAF96224 Human gen
51	13.8	69.0	24	4	AAH84143 Human cel
52	13.8	69.0	31	6	AAH84143 PCR prime
53	13.8	69.0	33	4	AAH84142 Human cel
54	13.8	69.0	45	4	AAH84141 Human cel
55	13.6	68.0	28	3	AAC81310 Mouse apo
56	13.6	68.0	37	2	AAX86699 Primer pH
57	13.6	68.0	49	3	AAX59078 Primer P3
58	13.4	67.0	45	12	ADO21826 PCR prime
59	13.4	67.0	49	12	ADO21825 PCR prime
60	13.2	66.0	20	6	AAV31181 Bacillus
61	13.2	66.0	20	6	ABK11827 Exchange
62	13.2	66.0	20	12	ADL35187 B. thurin
63	13.2	66.0	20	12	ADQ91981 pEG1089 p
64	13.2	66.0	21	13	ADQ04943 Cryptospor
65	13.2	66.0	24	10	ABZ80305 Mouse gpi
66	13.2	66.0	25	12	ADP03251 PCR prime
67	13.2	66.0	30	4	AAD13126 Human mem
68	13.2	66.0	33	4	AAD02560 Human ser
69	13.2	66.0	34	4	AAD13158 Human mem
70	13.2	66.0	34	4	AAD13146 Human MTS
71	13.2	66.0	40	6	ABZ45480 Human ATP
72	13.2	66.0	40	6	ABZ46886 Human ATP
73	13	65.0	37	10	ADR25786 PCR prime
74	12.8	64.0	19	12	ADQ62057 Anti-CD2
75	12.8	64.0	20	12	ADP85829 Mitochond
76	12.8	64.0	21	13	ADS34621 POSH prot
77	12.8	64.0	21	13	ADS34657 Y. 12/200
78	12.8	64.0	25	13	ADR55725 Drug ther
79	12.8	64.0	25	13	ADR55724 Drug ther
80	12.8	64.0	27	10	ADE15869 Fluoresce
81	12.8	64.0	39	10	ADD36629 Human pap
82	12.8	64.0	39	10	ADD22207 HPV E6 ge
83	12.8	64.0	47	3	AAX65855 Human map
84	12.8	64.0	47	3	AAX65896 Human map
85	12.8	64.0	48	2	AAQ80258 NDF prime
86	12.8	64.0	50	10	ADF44773 Artificial
87	12.6	63.0	20	10	ADC83994 Human pap
88	12.6	63.0	20	10	ADF43896 HPV 45 de
89	12.6	63.0	21	4	AAF97030 Human gen
90	12.6	63.0	24	2	AAV08436 SNUPE pri
91	12.6	63.0	24	2	AAV08437 SNUPE pri
92	12.6	63.0	25	9	ACI51890 Human mic
93	12.6	63.0	26	2	AAX05243 HIV-1 con

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:41:56 ; Search time 694.476 Seconds  
(without alignments)  
1395.446 Million cell updates/sec

Title: US-10-712-882A-8  
Perfect score: 20  
Sequence: 1 ttacatagccttcacg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

- 1: gb\_ba.\*
- 2: gb\_hcg.\*
- 3: gb\_in.\*
- 4: gb\_on.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sta.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	A82468 Sequence 6
2	20	100.0	20	6	I73226 Sequence 2
3	20	100.0	20	6	AR487076 Sequence
4	20	100.0	20	6	AR490516 Sequence
5	20	100.0	20	6	AR490518 Sequence
6	20	100.0	20	6	AR493821 Sequence
7	20	100.0	20	6	AR532953 Sequence
8	20	100.0	20	6	AR534175 Sequence
9	20	100.0	20	6	AR534191 Sequence
10	20	100.0	20	6	AR542782 Sequence
11	20	100.0	20	6	AX012488 Sequence
12	20	100.0	20	6	AX052804 Sequence
13	20	100.0	20	6	AX067277 Sequence
14	20	100.0	20	6	AX360020 Sequence
15	20	100.0	20	6	BD085846 Methods
16	20	100.0	20	6	BD124529 Predictio
17	18.4	92.0	21	6	AR112246 Sequence
18	18.4	92.0	21	6	AR112255 Sequence
19	18.4	92.0	25	6	AR112242 Sequence

20	18.4	92.0	25	6	AR112251 Sequence
21	18.4	92.0	26	6	AR112241 Sequence
22	18.4	92.0	26	6	AR112250 Sequence
23	18.4	92.0	27	6	AR112240 Sequence
24	18.4	92.0	27	6	AR112249 Sequence
25	18.4	92.0	28	6	AR112239 Sequence
26	18.4	92.0	28	6	AR112248 Sequence
27	18.4	92.0	29	6	AR112238 Sequence
28	18.4	92.0	29	6	AR112247 Sequence
29	18	90.0	19	6	AR112237 Sequence
30	17.4	87.0	23	6	AR112243 Sequence
31	17.4	87.0	23	6	AR112252 Sequence
32	16.4	82.0	21	6	AR112244 Sequence
33	16.4	82.0	21	6	AR112253 Sequence
34	15.2	76.0	36	6	AR7795 Sequence
35	15.2	76.0	36	6	AR218620 Sequence
36	14.4	72.0	17	6	AX723115 Sequence
37	14.4	72.0	18	6	AR112245 Sequence
38	14.4	72.0	18	6	AR112254 Sequence
39	14.4	72.0	20	6	AR230858 Sequence
40	14.2	71.0	20	6	BD184204 Sequence
41	14.2	71.0	20	6	AX742380 Sequence
42	14.2	71.0	33	6	AR138757 Sequence
43	14.2	71.0	33	6	AR176895 Sequence
44	14.2	71.0	33	6	I34696 Sequence
45	14.2	71.0	33	6	AR183646 Sequence
46	14.2	71.0	33	6	AR262727 Sequence
47	14.2	71.0	33	6	AX003994 Sequence
48	13.8	69.0	21	6	AR529786 Sequence
49	13.8	69.0	21	6	AX095811 Sequence
50	13.6	68.0	31	6	BD103450 Transform
51	13.6	68.0	28	6	BD004102 Apoptosis
52	13.6	68.0	32	9	HUMTCCVJ49
53	13.2	66.0	37	6	BD131641 Novel fun
54	13.2	66.0	20	6	AR107436 Sequence
55	13.2	66.0	20	6	AR156718 Sequence
56	13.2	66.0	20	6	AR166484 Sequence
57	13.2	66.0	20	6	AR179214 Sequence
58	13.2	66.0	20	6	AR282374 Sequence
59	13.2	66.0	20	6	AR301094 Sequence
60	13.2	66.0	20	6	AR429473 Sequence
61	13.2	66.0	20	6	AR490154 Sequence
62	13.2	66.0	20	6	AR544708 Sequence
63	13.2	66.0	20	6	AR383791 Sequence
64	13.2	66.0	20	6	BD007660 Delta-end
65	13.2	66.0	30	6	AX207916 Sequence
66	13.2	66.0	32	6	AX207944 Sequence
67	13.2	66.0	34	6	AX207936 Sequence
68	13.2	66.0	34	6	AX207949 Sequence
69	13.2	66.0	40	6	AX516066 Sequence
70	13.2	66.0	40	6	AX517472 Sequence
71	13	65.0	33	6	AX0019 SEQ ID NO:
72	13	65.0	33	6	I13207 Sequence 32
73	12.8	64.0	25	6	CQ864442 Sequence
74	12.8	64.0	25	6	CQ864443 Sequence
75	12.8	64.0	39	6	AX802743 Sequence
76	12.8	64.0	39	6	AX803126 Sequence
77	12.6	63.0	19	6	AI5088 Nucleotide
78	12.6	63.0	20	6	BD184274 Method an
79	12.6	63.0	24	6	AX742421 Sequence
80	12.6	63.0	24	6	AR063485 Sequence
81	12.6	63.0	24	6	AR063486 Sequence
82	12.6	63.0	25	6	AX610852 Sequence
83	12.6	63.0	26	6	AR078485 Sequence
84	12.6	63.0	26	6	AR152155 Sequence
85	12.6	63.0	35	6	AX938747 Sequence
86	12.6	63.0	38	6	AX933499 Sequence
87	12.6	63.0	38	6	AX933500 Sequence
88	12.6	63.0	42	6	I43946 Sequence 35
89	12.6	63.0	42	6	AX766986 Sequence
90	12.4	62.0	32	9	HUMTCCVJ49
91	12.4	62.0	47	6	AR288467 Sequence
92	12.4	62.0	47	6	AR288508 Sequence

Result No.	Score	Query #			ID	Description
		Match	Length	DB		
1	22	100.0	27	21	US-10-712-882-7	Sequence 7, Appli
2	22	100.0	27	10	US-09-888-056A-5	Sequence 5, Appli
3	22	100.0	27	15	US-10-167-227-29	Sequence 29, Appli
4	22	100.0	27	16	US-10-172-919-13	Sequence 13, Appli
5	22	100.0	27	20	US-10-823-197-13	Sequence 13, Appli
6	22	100.0	27	21	US-10-712-882-1	Sequence 1, Appli
7	22	100.0	27	21	US-10-712-882-9	Sequence 9, Appli





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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:46:26 ; Search time 1426.44 Seconds  
(without alignments)  
587.066 Million cell updates/sec

Title: US-10-712-882A-7

Perfect score: 22

Sequence: 1 tggctaccactgaactagc 22

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_ges1:\*

9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query: Match	Length	ID	Description
C 1	13.2	60.0	36	9	BM92503 Arabidops
C 2	12.8	58.2	44	4	BJ065975 BJ065975
C 3	12.6	57.3	46	9	CG800366 1118011A0
C 4	12.6	57.3	50	9	CR177236 Forward s
C 5	12.4	56.4	26	8	AZ779432 2M0015P14
C 6	12.4	56.4	43	9	BM660493 Arabidops
C 7	12.2	55.5	31	1	AU583675 tt74h06.x
C 8	12.2	55.5	44	1	AU254169 AU254169
C 9	12.2	54.5	34	1	AA8669975 vq10a06.i
C 10	12.2	54.5	43	1	AA445326 vf59h02.i
C 11	12.2	54.5	49	1	AT762609 w156d08.x
C 12	11.8	53.6	38	9	CG783331 0150530-0
C 13	11.8	53.6	45	8	AZ769358 1M0569M20
C 14	11.6	52.7	37	8	BZ593763 SALK_0820
C 15	11.6	52.7	37	8	CC053460 SALK_0435
C 16	11.6	52.7	40	9	U21495 U21495_Huma
C 17	11.6	52.7	45	1	AA794942 vr05903.i
C 18	11.6	52.7	48	1	AU243906 AU243906
C 19	11.4	51.8	30	8	AZ827644 2M0104N08
C 20	11.4	51.8	30	8	AZ958273 2M0225D05
C 21	11.4	51.8	34	7	T59625 YB66d05.s1
C 22	11.4	51.8	35	9	AJ587497 Arabidops
C 23	11.4	51.8	37	1	AI427510 mj63f10.x
C 24	11.4	51.8	38	9	CC885354 SALK_1469

AZ467036	1M0278109
AV833522	AV833522
AI082112	Cz38b10.8
BQ585750	E011419-0
AL939864	Arabidops
AZ315282	1M0032N31
CN973588	21092.60-
AZ763670	1M0559B16
AZ594734	1M0406119
BK655392	Arabidops
BZ663210	SALK_0268
BZ770906	SALK_1439
AZ973732	2M048M01
AZ592174	1M0402F21
AU102225	AU102225
AU102226	AU102226
AU102229	AU102229
AU102232	AU102232
AU102233	AU102233
AU102234	AU102234
AU102237	AU102237
AU102239	AU102239
AU104955	AU104955
AU104956	AU104956
AU104957	AU104957
AU104958	AU104958
AU104960	AU104960
AU104961	AU104961
AU104963	AU104963
AU104965	AU104965
AU270588	AU270588
CO730398	SnESTbaa2
CR359782	Arabidops
CL656662	PR10127a
AZ826719	1M0467E07
AZ466667	1M0277G06
AZ839538	2M0135F10
AL474370	T. brucei
AZ769374	1M0570A02
CR403281	Arabidops
BJ064687	BJ064687
BH861169	SALK_0346
AJ304156	Plasmodi
AZ591824	1M0402K07
BZ289706	SALK_0231
AL937939	Arabidops
AI496779	fb61c01.y
AL945128	Arabidops
BH905827	SALK_1078
AI035452	ub47507.r
AZ855607	2M0159A13
BH906956	SALK_0368
EX184327	DaniO_rer
AI262384	GK37all.x
AZ864345	2M0173F19
CL865899	AL0248 Sa
BZ591745	3590.1.64
AZ311328	1M0026G12
CC326500	XN701 Bay
BZ378492	SALK_1081
AU006473	AU006473
AW496816	1G1 Neuro
AZ576556	ACT-T11C0
BH903249	SALK_1023
CG918523	01S0458-0
AU104873	AU104873
AU104880	AU104880
AU104904	AU104904
AU105837	AU105837
AU107286	AU107286
CR437050	CR437050
AZ635616	1M0495C18
CC516471	CH240_362

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 16:54:30 ; Search time 190.352 Seconds  
(without alignments)  
684.175 Million cell updates/sec

Title: US-10-712-882A-7

Perfect score: 22

Sequence: 1 tggctaccacctaactaggc 22

Scoring table: IDENTITY NUC

Gapex 10.0, Gapex 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: N\_Geneseq\_16Dec04:\*  
2: Geneseqm1980s:\*  
3: Geneseqm1990s:\*  
4: Geneseqm2000s:\*  
5: Geneseqm2001as:\*  
6: Geneseqm2001bs:\*  
7: Geneseqm2002as:\*  
8: Geneseqm2002bs:\*  
9: Geneseqm2003as:\*  
10: Geneseqm2003bs:\*  
11: Geneseqm2003ds:\*  
12: Geneseqm2004as:\*  
13: Geneseqm2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	2	AAT70316 Primer fo
2	22	100.0	22	3	Aaz37202 PCR prime
3	22	100.0	22	3	AAC63024 Human IL-
4	22	100.0	27	2	Aav32389 Interleuk
5	22	100.0	27	2	Aaz10700 PCR prime
6	22	100.0	27	2	Aax75921 Human int
7	22	100.0	27	3	Aaz37218 PCR prime
8	22	100.0	27	3	AAC63004 Human IL-
9	22	100.0	27	5	AAC91431 Human IL-
10	22	100.0	27	6	AAD27381 PCR prime
11	22	100.0	27	8	AAL54507 Ageing-re
12	22	100.0	27	10	AAD51461 Human int
13	22	100.0	27	12	ADL83335 PCR prime
14	22	100.0	27	12	ADN48852 Human int
15	22	100.0	27	12	ADQ35280 Human int
16	21	95.5	21	2	AAAI6611 Interleuk
17	21	95.5	21	2	ABX15539 Human IL-
18	21	95.5	21	9	Aaf27676 Primer #9
19	16.8	76.4	25	9	ACK18778 Human mic
20	15.8	71.8	47	3	Aaz67066 Human map

C	21	15.2	69.1	25	9	ACK18779 Human mic
	22	14.8	67.3	20	2	AAQ28501 Polymeras
	23	14.6	66.4	25	9	ACI78440 Human mic
	24	14.6	66.4	25	9	ACI77838 Human mic
	25	14.2	64.5	19	2	AAV32395 Interleuk
	26	14.2	64.5	38	4	AA76985 Human G p
	27	14.2	64.5	42	12	ADM36323 Bacteriop
	28	14.2	64.5	50	4	AAU32458 Human SNP
	29	14	63.7	41	4	AAI66442 DBH and P
	30	13.8	62.7	19	2	AAT96922 Human pRB
	31	13.6	61.8	20	6	AAI72107 PGL-VFR f
	32	13.6	61.8	23	12	ADJ57664 Primer of
	33	13.6	61.8	25	9	ACI95662 Human mic
	34	13.6	61.8	25	9	ACI95663 Human mic
	35	13.6	61.8	50	6	ABZ07241 Human leu
	36	13.4	60.9	21	10	ADD14293 Human src
	37	13.4	60.9	21	12	ADM10351 Human cyp
	38	13.4	60.9	24	6	ABZ31657 Candida a
	39	13.4	60.9	25	9	ACK03316 Human mic
	40	13.4	60.9	25	9	ACK02690 Human mic
	41	13.2	60.0	25	9	ACK02443 Human mic
	42	13.2	60.0	25	9	ACK11667 Human mic
	43	13.2	60.0	27	3	AAAI2765 PCR prime
	44	13.2	60.0	27	4	AAAD02759 Gene spec
	45	13.2	60.0	27	6	AAZ32587 RACE prim
	46	13.2	60.0	27	11	ADL95406 Angiotens
	47	13	59.1	25	9	ACI77839 Human mic
	48	13	59.1	25	9	ACI78441 Human mic
	49	13	59.1	25	9	ACH56236 DNA targe
	50	13	59.1	33	4	AH446270 Human iro
	51	13	59.1	33	6	ABV75444 Human tra
	52	13	59.1	40	3	AAZ61078 PCR prime
	53	13	59.1	40	3	AAZ61074 PCR prime
	54	13	59.1	40	4	AAAI7965 A. fumiga
	55	13	59.1	41	4	AAI65346 Human diH
	56	13	59.1	47	3	AAZ68591 Human map
	57	13	59.1	47	3	AAZ61076 PCR prime
	58	13	59.1	50	4	AAU34269 Human SNP
	59	12.8	58.2	20	10	ADF17820 Sequencin
	60	12.8	58.2	24	10	ACF58471 M. hyorhi
	61	12.8	58.2	25	9	ACI32723 Human mic
	62	12.8	58.2	25	9	ACI45209 Human mic
	63	12.8	58.2	25	9	ACI14330 Human mic
	64	12.8	58.2	25	9	ACI32722 Human mic
	65	12.8	58.2	25	9	ACI83745 Human mic
	66	12.8	58.2	25	9	ACI93358 Human mic
	67	12.8	58.2	27	2	AAV11545 Recombina
	68	12.8	58.2	29	2	AAZ80487 Human sec
	69	12.8	58.2	29	4	AAZ59322 Human sec
	70	12.8	58.2	29	6	ABA90991 Biotinyla
	71	12.8	58.2	30	6	ABX10842 Cholecyst
	72	12.8	58.2	38	2	AAV27449 Streptoco
	73	12.8	58.2	38	6	ABQ84917 Streptoco
	74	12.8	58.2	38	6	ABQ84917 Streptoco
	75	12.8	58.2	38	10	ADC45320 S. pneumo
	76	12.8	58.2	46	1	AAZ0864 Granulocy
	77	12.6	57.3	20	5	AAZ01090 Human leu
	78	12.6	57.3	20	2	AAZ33211 Alpha-Amy
	79	12.6	57.3	20	9	AAZ55996 PGL3-Mxa
	80	12.6	57.3	20	9	AAI61400 Human FXR
	81	12.6	57.3	20	12	ADOS4049 Farnesoid
	82	12.6	57.3	20	12	ADOS4074 Farnesoid
	83	12.6	57.3	23	3	AAZ58539 Arabidops
	84	12.6	57.3	23	4	AAH23728 PCR prime
	85	12.6	57.3	25	6	ABN05604 Human GDM
	86	12.6	57.3	25	6	ABN05602 Human GDM
	87	12.6	57.3	25	6	ABN05603 Human GDM
	88	12.6	57.3	25	6	ABN05605 Human GDM
	89	12.6	57.3	25	6	ABN05608 Human GDM
	90	12.6	57.3	25	6	ABN05607 Human GDM
	91	12.6	57.3	25	6	ABN05606 Human GDM
	92	12.6	57.3	25	9	ACI39102 Human mic
	93	12.6	57.3	25	9	ACI57422 Human mic
	93	12.6	57.3	25	9	ACK04872 Human mic

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:41:56 ; Search time 763.924 Seconds  
(without alignments)  
1395.446 Million cell updates/sec

Title: US-10-712-882A-7  
Perfect score: 22  
Sequence: 1 ttttaccacctgaactagc 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	AR112256	AR112256 Sequence
2	22	100.0	22	I73225	I73225 Sequence 1
3	22	100.0	22	AR490515	AR490515 Sequence
4	22	100.0	22	AR534174	AR534174 Sequence
5	22	100.0	27	AR112236	AR112236 Sequence
6	22	100.0	27	AR490509	AR490509 Sequence
7	22	100.0	27	AR490517	AR490517 Sequence
8	22	100.0	27	AR493820	AR493820 Sequence
9	22	100.0	27	AR532952	AR532952 Sequence
10	22	100.0	27	AR534190	AR534190 Sequence
11	22	100.0	27	AR542781	AR542781 Sequence
12	22	100.0	27	AX012487	AX012487 Sequence
13	22	100.0	27	AX052803	AX052803 Sequence
14	22	100.0	27	AX360019	AX360019 Sequence
15	22	100.0	27	BD085845	BD085845 Methods o
16	21	95.5	21	A82467	A82467 Sequence 5
17	21	95.5	21	AR487075	AR487075 Sequence
18	21	95.5	21	AX067276	AX067276 Sequence
19	21	95.5	21	BD124528	BD124528 Predictio

C	20	15.8	71.8	47	6	AR289678	AR289678 Sequence
C	21	14.8	67.3	20	6	I13552	I13552 Sequence 2
C	22	14.2	64.5	38	6	BD012991	BD012991 Novel G p
C	23	14.2	64.5	38	6	BD014502	BD014502 Novel G p
C	24	14.2	64.5	39	6	AR050328	AR050328 Sequence
C	25	14.2	64.5	50	6	CQ007026	CQ007026 Sequence
C	26	14	63.6	42	10	AB002263	AB002263 Mus muscu
C	27	14	63.6	49	4	FCU1RNA	Y14154 Felis catus
C	28	13.8	62.7	19	6	AR038723	AR038723 Sequence
C	29	13.8	62.7	19	6	AR059609	AR059609 Sequence
C	30	13.6	61.8	20	6	AX131716	AX131716 Sequence
C	31	13.4	60.9	24	6	AX488576	AX488576 Sequence
C	32	13.2	60.0	27	6	AR135179	AR135179 Sequence
C	33	13.2	60.0	27	6	BD274686	BD274686 Angiotens
C	34	13.2	60.0	27	6	AR382343	AR382343 Sequence
C	35	13.2	60.0	27	6	AX418994	AX418994 Sequence
C	36	13	59.1	31	6	I92393	I92393 Sequence 45
C	37	13	59.1	31	6	I92395	I92395 Sequence 47
C	38	13	59.1	40	6	BD245071	BD245071 Regions o
C	39	13	59.1	40	6	BD245075	BD245075 Regions o
C	40	13	59.1	47	6	BD245073	BD245073 Regions o
C	41	13	59.1	47	6	AR291205	AR291205 Sequence
C	42	13	59.1	50	6	CQ008837	CQ008837 Sequence
C	43	12.8	58.2	20	6	AX815394	AX815394 Sequence
C	44	12.8	58.2	28	6	CQ794117	CQ794117 Sequence
C	45	12.8	58.2	28	6	CQ800086	CQ800086 Sequence
C	46	12.8	58.2	30	6	BD123462	BD123462 Method of
C	47	12.8	58.2	36	6	I03354	I03354 Sequence 4
C	48	12.8	58.2	38	6	AR120363	AR120363 Sequence
C	49	12.8	58.2	38	6	AR341054	AR341054 Sequence
C	50	12.8	58.2	38	6	BD063372	BD063372 Streptoco
C	51	12.8	58.2	42	6	A01539	A01539 Oligonucleo
C	52	12.8	58.2	46	9	H0MCD3E04	M23320 Human membr
C	53	12.6	57.3	20	6	E64493	E64493 Sugar-respo
C	54	12.6	57.3	21	6	AR529966	AR529966 Sequence
C	55	12.6	57.3	21	6	AX095991	AX095991 Sequence
C	56	12.6	57.3	23	6	E51347	E51347 p73 promote
C	57	12.6	57.3	23	6	AR532593	AR532593 Sequence
C	58	12.6	57.3	25	6	CQ620854	CQ620854 Sequence
C	59	12.6	57.3	25	6	CQ620855	CQ620855 Sequence
C	60	12.6	57.3	25	6	CQ620856	CQ620856 Sequence
C	61	12.6	57.3	25	6	CQ620857	CQ620857 Sequence
C	62	12.6	57.3	25	6	CQ620858	CQ620858 Sequence
C	63	12.6	57.3	25	6	CQ620859	CQ620859 Sequence
C	64	12.6	57.3	25	6	CQ620860	CQ620860 Sequence
C	65	12.6	57.3	25	6	CQ861850	CQ861850 Sequence
C	66	12.6	57.3	25	6	AR461917	AR461917 Sequence
C	67	12.6	57.3	25	6	AR461918	AR461918 Sequence
C	68	12.6	57.3	25	6	AR461919	AR461919 Sequence
C	69	12.6	57.3	25	6	AR461920	AR461920 Sequence
C	70	12.6	57.3	25	6	AR461921	AR461921 Sequence
C	71	12.6	57.3	25	6	AR461922	AR461922 Sequence
C	72	12.6	57.3	25	6	AR461923	AR461923 Sequence
C	73	12.6	57.3	25	6	AR371728	AR371728 Sequence
C	74	12.6	57.3	27	6	BD086192	BD086192 Chemokine
C	75	12.6	57.3	29	6	BD190753	BD190753 Secreted
C	76	12.6	57.3	29	6	I16005	I16005 Sequence 8
C	77	12.6	57.3	29	6	AX099574	AX099574 Sequence
C	78	12.6	57.3	30	6	AR232925	AR232925 Sequence
C	79	12.6	57.3	30	6	AR275642	AR275642 Sequence
C	80	12.6	57.3	30	6	AX235917	AX235917 Sequence
C	81	12.6	57.3	30	6	AX357361	AX357361 Sequence
C	82	12.6	57.3	30	6	AX551118	AX551118 Sequence
C	83	12.6	57.3	30	6	AX551818	AX551818 Sequence
C	84	12.6	57.3	31	6	E44155	E44155 Novel G pro
C	85	12.6	57.3	31	6	AX463680	AX463680 Sequence
C	86	12.6	57.3	35	11	C75850	C75850 Homo sapien
C	87	12.6	57.3	36	6	E44150	E44150 Novel G pro
C	88	12.6	57.3	42	6	AX551246	AX551246 Sequence
C	89	12.6	57.3	42	6	AX551946	AX551946 Sequence
C	90	12.6	57.3	50	6	CQ006784	CQ006784 Sequence
C	91	12.6	57.3	50	6	AR359019	AR359019 Sequence
C	92	12.6	57.3	50	6	AR540575	AR540575 Sequence



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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:11:51 ; Search time 41.6905 Seconds  
(without alignments)  
667.220 Million cell updates/sec

Title: US-10-712-882A-6

Perfect score: 17

Sequence: 1 tcttggtcgcaggtaa 17

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA.\*

1: /cgm2\_6/prodata/1/ina/5A COMB.seq.\*

2: /cgm2\_6/prodata/1/ina/5B COMB.seq.\*

3: /cgm2\_6/prodata/1/ina/6A COMB.seq.\*

4: /cgm2\_6/prodata/1/ina/6B COMB.seq.\*

5: /cgm2\_6/prodata/1/ina/PCTUS COMB.seq.\*

6: /cgm2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	1	US-08-628-282-2
2	17	100.0	17	2	US-08-587-911-2
3	17	100.0	17	3	US-08-813-456-2
4	17	100.0	17	4	US-09-345-217-23
5	17	100.0	17	5	US-09-431-352-2
6	17	100.0	17	6	US-09-845-129-23
7	17	100.0	17	7	US-09-037-472-6
8	17	100.0	17	8	US-09-632-657-10
9	17	100.0	17	9	US-09-693-555A-16
10	15.4	90.6	17	4	US-09-578-534-8
11	13.4	78.8	25	4	US-09-396-1966-70428
12	13.4	78.8	25	4	US-09-396-1966-70429
13	13	76.5	16	4	US-09-584-950-14
14	13	76.5	45	2	US-08-944-982-1
15	12.8	75.3	25	4	US-09-396-1966-3135
16	12.8	75.3	25	4	US-09-396-1966-3136
17	12.8	75.3	25	4	US-09-396-1966-12523
18	12.8	75.3	25	4	US-09-396-1966-26322
19	12.8	75.3	25	4	US-09-396-1966-71931
20	12.8	75.3	25	4	US-09-396-1966-71932
21	12.8	75.3	25	4	US-09-105-907-4
22	12.8	75.3	27	3	US-09-578-378-4
23	12.8	75.3	47	4	US-09-422-978-960
24	12.4	72.9	22	4	US-09-079-723-156
25	12.4	72.9	29	4	US-09-304-232-801
26	12.4	72.9	40	3	US-09-485-737B-16
27	12.4	72.9	40	3	US-09-485-737B-17

40	4	US-10-071-485-16	72.9	12.4	28	Sequence 16, Appl
40	4	US-10-071-485-17	72.9	12.4	29	Sequence 17, Appl
19	1	US-08-439-962-9	71.8	12.2	30	Sequence 9, Appl
19	2	US-08-497-535-9	71.8	12.2	31	Sequence 9, Appl
19	2	US-09-098-317-9	71.8	12.2	32	Sequence 9, Appl
19	3	US-09-323-555B-9	71.8	12.2	33	Sequence 9, Appl
19	3	US-09-323-555B-14	71.8	12.2	34	Sequence 9, Appl
19	5	PCT-US96-06666-9	71.8	12.2	35	Sequence 14, Appl
24	4	US-09-815-585-24	71.8	12.2	36	Sequence 24, Appl
25	4	US-09-396-1966G-1212	71.8	12.2	37	Sequence 1212, Ap
25	4	US-09-396-1966G-42026	71.8	12.2	38	Sequence 42026, A
25	4	US-09-396-1966G-42027	71.8	12.2	39	Sequence 42027, A
25	4	US-09-396-1966G-57217	71.8	12.2	40	Sequence 57217, A
25	4	US-09-396-1966G-57234	71.8	12.2	41	Sequence 57234, A
25	4	US-09-396-1966G-124435	71.8	12.2	42	Sequence 124435, A
25	4	US-09-396-1966G-124436	71.8	12.2	43	Sequence 124436, A
30	3	US-09-123-030-5	71.8	12.2	44	Sequence 5, Appl
20	3	US-09-011-479-1	70.6	12	45	Sequence 1, Appl
25	4	US-09-396-1966G-33100	70.6	12	46	Sequence 33100, A
17	3	US-08-985-162-232	69.4	11.8	47	Sequence 232, App
18	4	US-09-401-063-232	69.4	11.8	48	Sequence 232, App
18	4	US-09-171-937C-57	69.4	11.8	49	Sequence 57, Appl
20	3	US-09-288-461-92	69.4	11.8	50	Sequence 92, Appl
20	3	US-09-429-322-46	69.4	11.8	51	Sequence 46, Appl
20	4	US-09-758-881-92	69.4	11.8	52	Sequence 92, Appl
25	4	US-09-396-1966G-36851	69.4	11.8	53	Sequence 36851, A
25	4	US-09-396-1966G-31025	69.4	11.8	54	Sequence 31025, A
25	4	US-09-396-1966G-32941	69.4	11.8	55	Sequence 32941, A
25	4	US-09-396-1966G-37527	69.4	11.8	56	Sequence 37527, A
25	4	US-09-396-1966G-54337	69.4	11.8	57	Sequence 54337, A
25	4	US-09-396-1966G-54338	69.4	11.8	58	Sequence 54338, A
25	4	US-09-396-1966G-54339	69.4	11.8	59	Sequence 54339, A
25	4	US-09-396-1966G-54340	69.4	11.8	60	Sequence 54340, A
25	4	US-09-396-1966G-58823	69.4	11.8	61	Sequence 58823, A
25	4	US-09-396-1966G-74540	69.4	11.8	62	Sequence 74540, A
25	4	US-09-396-1966G-124468	69.4	11.8	63	Sequence 124468, A
25	4	US-09-396-1966G-124437	69.4	11.8	64	Sequence 124437, A
32	4	US-09-462-843A-13	69.4	11.8	65	Sequence 13, Appl
36	1	US-07-936-421-15	69.4	11.8	66	Sequence 15, Appl
47	3	US-09-641-638-992	69.4	11.8	67	Sequence 992, App
47	4	US-09-422-978-579	69.4	11.8	68	Sequence 579, App
47	4	US-10-170-097-992	69.4	11.8	69	Sequence 992, App
48	1	US-08-381-572-4	69.4	11.8	70	Sequence 4, Appl
49	1	US-08-592-820-4	69.4	11.8	71	Sequence 4, Appl
49	1	US-08-171-389-49	69.4	11.8	72	Sequence 49, Appl
49	1	US-08-171-389-50	69.4	11.8	73	Sequence 49, Appl
49	1	US-08-123-936-49	69.4	11.8	74	Sequence 49, Appl
49	1	US-08-123-936-50	69.4	11.8	75	Sequence 49, Appl
49	2	US-08-475-228A-49	69.4	11.8	76	Sequence 49, Appl
49	2	US-08-475-228A-50	69.4	11.8	77	Sequence 49, Appl
49	3	US-08-482-080A-49	69.4	11.8	78	Sequence 49, Appl
49	3	US-08-482-080A-50	69.4	11.8	79	Sequence 49, Appl
49	3	US-09-354-947-49	69.4	11.8	80	Sequence 49, Appl
49	3	US-09-538-709-1150	69.4	11.8	81	Sequence 49, Appl
49	5	PCT-US93-12388-49	69.4	11.8	82	Sequence 49, Appl
49	5	PCT-US93-12388-50	69.4	11.8	83	Sequence 49, Appl
50	1	US-08-171-389-52	69.4	11.8	84	Sequence 50, Appl
50	1	US-08-123-936-52	69.4	11.8	85	Sequence 50, Appl
50	2	US-08-475-228A-52	69.4	11.8	86	Sequence 52, Appl
50	3	US-08-482-080A-52	69.4	11.8	87	Sequence 52, Appl
50	3	US-09-354-947-52	69.4	11.8	88	Sequence 52, Appl
50	5	PCT-US93-12388-52	69.4	11.8	89	Sequence 52, Appl
18	3	US-09-341-587-9	67.1	11.4	90	Sequence 52, Appl
20	3	US-09-393-529-15	67.1	11.4	91	Sequence 9, Appl
20	3	US-09-907-843-45	67.1	11.4	92	Sequence 15, Appl
20	4	US-09-515-721-1	67.1	11.4	93	Sequence 45, Appl
21	3	US-09-131-956-4	67.1	11.4	94	Sequence 1, Appl
21	4	US-09-657-472-85	67.1	11.4	95	Sequence 4, Appl
21	4	US-09-657-472-2182	67.1	11.4	96	Sequence 85, Appl
22	1	US-08-485-618-94	67.1	11.4	97	Sequence 2182, Ap
22	1	US-08-605-672-94	67.1	11.4	98	Sequence 94, Appl
22	2	US-08-482-293A-94	67.1	11.4	99	Sequence 94, Appl
22	2		67.1	11.4	100	

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:46:26 ; Search time 1102.25 Seconds  
(without alignments)  
587.066 Million cell updates/sec

Title: US-10-712-882A-6  
Perfect score: 17  
Sequence: 1 tcctggtctgcaggtaa 17

Scoring table: IDENTITY NUC  
Gap 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

- EST:\*
- 1: gb\_est1:\*
  - 2: gb\_est2:\*
  - 3: gb\_hcc:\*
  - 4: gb\_est3:\*
  - 5: gb\_est4:\*
  - 6: gb\_est5:\*
  - 7: gb\_est6:\*
  - 8: gb\_gse1:\*
  - 9: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.4	78.8	31	4	BJ028740
2	12.8	75.3	31	1	AV832744
3	12.4	72.9	35	8	AZ332622
4	12.4	72.9	43	1	AA510887
5	12.4	72.9	47	1	AV948056
6	12.2	71.8	39	9	AG194707
7	12.2	71.8	50	8	AZ330881
8	11.8	69.4	19	1	AI016864
9	11.8	69.4	44	9	CL233849
10	11.8	69.4	45	2	AV950015
11	11.8	69.4	46	9	CL234601
12	11.4	67.1	41	9	BX121769
13	11.4	67.1	44	2	AV952892
14	11.4	67.1	46	8	AZ937852
15	11.4	67.1	47	2	AV971035
16	11.4	67.1	49	1	AA681251
17	11.2	65.9	33	8	AZ665095
18	11.2	65.9	40	8	AZ622990
19	11.2	65.9	50	1	AU107940
20	11.1	64.7	31	8	AZ440093
21	11.1	64.7	36	4	BG927976
22	11.1	64.7	43	1	AV832522
23	11.1	64.7	43	4	BJ060427
24	11.1	64.7	44	4	BJ039583

25	64.7	11	45	2	AV959772
26	64.7	11	45	2	AV959863
27	64.7	11	45	2	AV962463
28	64.7	11	45	4	BJ057980
29	64.7	11	48	4	BJ030281
30	64.7	11	49	1	AV947763
31	10.8	63.5	20	8	AZ938837
32	10.8	63.5	24	8	AZ812707
33	10.8	63.5	37	1	AI093617
34	10.8	63.5	42	8	BH789425
35	10.8	63.5	43	8	AZ387876
36	10.8	63.5	43	9	CL002097
37	10.8	63.5	43	9	CL234584
38	10.8	63.5	44	8	AZ980367
39	10.8	63.5	46	1	AA485011
40	10.8	63.5	46	1	AA604908
41	10.8	63.5	46	8	AZ812990
42	10.8	63.5	47	1	AJ666278
43	10.8	63.5	48	8	AZ485794
44	10.8	63.5	50	1	AA534091
45	10.8	63.5	50	1	AU106349
46	10.6	62.4	26	9	CL657414
47	10.6	62.4	31	9	CL211500
48	10.6	62.4	35	9	CG400280
49	10.6	62.4	41	9	AG191947
50	10.6	62.4	45	1	AJ792767
51	10.6	62.4	46	8	CL183613
52	10.6	62.4	49	1	AI680337
53	10.6	62.4	49	1	BI316972
54	10.6	62.4	49	9	BM95877
55	10.6	62.4	50	1	AU103958
56	10.6	62.4	50	1	AU104046
57	10.6	62.4	50	8	AZ308311
58	10.4	61.2	22	8	AZ833042
59	10.4	61.2	28	8	AZ626780
60	10.4	61.2	29	8	AZ643111
61	10.4	61.2	31	1	AA222609
62	10.4	61.2	31	8	AZ468300
63	10.4	61.2	31	8	AZ837229
64	10.4	61.2	32	8	AZ837229
65	10.4	61.2	37	1	AA982394
66	10.4	61.2	39	9	CC800059
67	10.4	61.2	39	9	CG892116
68	10.4	61.2	39	9	CL002872
69	10.4	61.2	40	8	AZ823116
70	10.4	61.2	40	8	AZ002899
71	10.4	61.2	40	9	CL002909
72	10.4	61.2	41	8	AZ463683
73	10.4	61.2	41	8	CC180419
74	10.4	61.2	41	9	CL002870
75	10.4	61.2	41	9	CL234265
76	10.4	61.2	42	4	BI819090
77	10.4	61.2	42	9	CL002482
78	10.4	61.2	44	9	CG847080
79	10.4	61.2	44	9	CL234775
80	10.4	61.2	45	1	AV947576
81	10.4	61.2	45	9	CL002904
82	10.4	61.2	46	9	CG18674
83	10.4	61.2	47	9	CG18674
84	10.4	61.2	47	9	CG18674
85	10.4	61.2	48	8	BH857725
86	10.4	61.2	49	9	CL002706
87	10.4	61.2	50	2	AV955523
88	10.4	61.2	50	9	AL952981
89	10.2	60.0	25	1	AL952981
90	10.2	60.0	28	7	CF305592
91	10.2	60.0	30	1	BI907635
92	10.2	60.0	31	1	AI323319
93	10.2	60.0	34	1	AI191436
94	10.2	60.0	36	9	BM93425
95	10.2	60.0	37	1	AA911865
96	10.2	60.0	37	8	AZ503971
97	10.2	60.0	38	9	CL214453

AV959772	AV959772
AV959863	AV959863
AV962463	AV962463
BJ057980	BJ057980
BJ030281	BJ030281
AV947763	AV947763
AZ938837	AZ938837
AZ812707	AZ812707
AI093617	AI093617
BH789425	BH789425
AZ387876	AZ387876
CL002097	CL002097
CL234584	CL234584
AZ980367	AZ980367
AA485011	AA485011
AA604908	AA604908
AZ812990	AZ812990
AJ666278	AJ666278
AZ485794	AZ485794
AA534091	AA534091
AU106349	AU106349
AU107094	AU107094
CL657414	CL657414
CL211500	CL211500
CG400280	CG400280
AG191947	AG191947
AJ792767	AJ792767
CL183613	CL183613
AI680337	AI680337
BI316972	BI316972
BM95877	BM95877
AU103958	AU103958
AU104046	AU104046
AZ308311	AZ308311
AZ833042	AZ833042
AZ626780	AZ626780
AZ643111	AZ643111
AA222609	AA222609
AZ468300	AZ468300
AZ837229	AZ837229
AA982394	AA982394
CC800059	CC800059
CG892116	CG892116
CL002872	CL002872
AZ823116	AZ823116
AZ002899	AZ002899
CL002909	CL002909
AZ463683	AZ463683
CC180419	CC180419
CL002870	CL002870
CL234265	CL234265
BI819090	BI819090
CL002482	CL002482
CG847080	CG847080
CL234775	CL234775
AV947576	AV947576
CL002904	CL002904
CG18674	CG18674
CL234529	CL234529
BH857725	BH857725
CL002706	CL002706
AV955523	AV955523
AL952981	AL952981
AL952981	AL952981
CF305592	CF305592
BI907635	BI907635
AI323319	AI323319
AI191436	AI191436
BM93425	BM93425
AA911865	AA911865
AZ503971	AZ503971
CL214453	CL214453

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 16:54:30 ; Search time 147.09 Seconds  
(without alignments)  
684.175 Million cell updates/sec

Title: US-10-712-882A-6  
Perfect score: 17  
Sequence: 1 tctgggtcgcaggtaa 17

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: Geneseq19808:\*  
2: Geneseq19908:\*  
3: Geneseq20008:\*  
4: Geneseq20018:\*  
5: Geneseq20028:\*  
6: Geneseq20038:\*  
7: Geneseq20048:\*  
8: Geneseq20058:\*  
9: Geneseq20068:\*  
10: Geneseq20078:\*  
11: Geneseq20088:\*  
12: Geneseq20098:\*  
13: Geneseq20108:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	2	AAT89948 Human Int
2	17	100.0	17	2	AAT89410 Human IL-
3	17	100.0	17	2	AAV62391 IL-1 rece
4	17	100.0	17	2	AAV60231 PCR prime
5	17	100.0	17	2	AAV32394 Interleuk
6	17	100.0	17	2	AAX10707 PCR prime
7	17	100.0	17	2	AAX16622 Interleuk
8	17	100.0	17	2	ABX15550 Human IL-
9	17	100.0	17	3	AAZ37217 PCR prime
10	17	100.0	17	3	AAAG1916 Human IL-
11	17	100.0	17	3	AAC63788 Human IL-
12	17	100.0	17	4	AAF27687 Primer #2
13	17	100.0	17	5	AAC89172 Human IL-
14	17	100.0	17	6	AAD27378 PCR prime
15	17	100.0	17	8	AAL54514 Ageing-re
16	17	100.0	17	12	ADN48847 Human sec
17	15.4	90.6	17	2	AAX75918 Human int
18	15.4	90.6	17	5	AAC91426 Human IL-
19	15.4	90.6	17	8	AAL54502 Ageing-re
20	15.4	90.6	17	10	AAD51456 Human int

21	15.4	90.6	17	12	ADL83330	Adl83330 PCR prime
22	13.4	78.8	20	4	AAT27330	Aat27330 Human TSG
23	13.4	78.8	21	6	ABS60580	Abs60580 Human pol
24	13	76.5	16	12	ADO35277	Ado35277 Human inh
25	13	76.5	20	9	AAL61527	Aal61527 Human tie
26	13	76.5	23	2	AAQ90371	Aaq90371 Mouse tie
27	13	76.5	27	10	ADP36108	Adp36108 Sma3002-d
28	13	76.5	27	10	ADP36109	Adp36109 Sma3002-d
29	13	76.5	45	2	AAX06652	Aax06652 CTP gene
30	13	76.5	50	4	AAL33605	Aal33605 Human SNP
31	12.8	75.3	20	9	ADP74452	Adp74452 Human NRF
32	12.8	75.3	20	12	ADP74452	Adp74452 Human NRF
33	12.8	75.3	20	12	ADP74522	Adp74522 Human neu
34	12.8	75.3	21	6	AAL48162	Aal48162 Human epp
35	12.8	75.3	24	4	AAD21443	Aad21443 Human mic
36	12.8	75.3	25	9	ACK17693	Ack17693 Human mic
37	12.8	75.3	27	3	AAX49175	Aax49175 PCR prime
38	12.8	75.3	30	8	ACA60842	Aca60842 Human DNA
39	12.8	75.3	40	2	AAT70634	Aat70634 Fibrin cl
40	12.8	75.3	47	3	AAX66613	Aax66613 Human map
41	12.8	75.3	48	6	ABK22559	Abk22559 Human ERG
42	12.8	75.3	50	4	AAL34228	Aal34228 Human SNP
43	12.4	72.9	17	2	AAA22665	Aaa22665 Integrin
44	12.4	72.9	20	10	ADC98347	Adc98347 ACLP02 po
45	12.4	72.9	20	10	ADC98351	Adc98351 ACLP07 po
46	12.4	72.9	22	2	AAX18158	Aax18158 GI tract
47	12.4	72.9	22	6	ABU44612	Abu44612 Human chr
48	12.4	72.9	25	9	ACI69315	Act69315 Human mic
49	12.4	72.9	25	9	ACI68697	Act68697 Human mic
50	12.4	72.9	29	3	AAA04601	Aaa04601 Polymorph
51	12.4	72.9	30	12	ADN07683	Adn07683 KIAA1855
52	12.4	72.9	38	12	ADM28599	Adm28599 Pan-funga
53	12.4	72.9	40	2	AAX08544	Aax08544 Oligonuc1
54	12.4	72.9	40	2	AAX08545	Aax08545 Oligonuc1
55	12.4	72.9	41	8	ABX75270	Abx75270 Human gen
56	12.4	72.9	41	12	ADJ37015	Adj37015 Gene 216
57	12.4	72.9	41	12	ADL81593	Adl81593 Gene 216
58	12.4	72.9	48	11	ADL76169	Adl76169 Human PTC
59	12.4	72.9	50	4	AAL30340	Aal30340 Human SNP
60	12.2	71.8	19	2	AAT43184	Aat43184 Primary t
61	12.2	71.8	19	2	AAT43182	Aat43182 Cell prol
62	12.2	71.8	20	6	ABI95252	Abi95252 Capture o
63	12.2	71.8	20	11	ADP75383	Adp75383 Human ADA
64	12.2	71.8	23	2	AAQ67681	Aaq67681 Protein t
65	12.2	71.8	24	4	AAL65493	Aal65493 Probe for
66	12.2	71.8	24	6	AAL66242	Aal66242 Molecular
67	12.2	71.8	24	6	ABI87075	Abi87075 Capture o
68	12.2	71.8	24	6	ABI87074	Abi87074 Capture o
69	12.2	71.8	24	10	ADC39272	Adc39272 Novel hum
70	12.2	71.8	24	10	ADE28046	Adc28046 Linear pr
71	12.2	71.8	25	9	ACK24771	Ack24771 Human mic
72	12.2	71.8	29	13	ADR88860	Adr88860 Antibody-
73	12.2	71.8	30	6	ABX51911	Abx51911 Mouse clo
74	12.2	71.8	30	12	ADG25229	Adg25229 Human Cys
75	12.2	71.8	31	4	AAL30460	Aal30460 Human sin
76	12.2	71.8	31	6	ABQ79035	Abq79035 Human Tcf
77	12.2	71.8	33	13	ADR88874	Adr88874 Antibody-
78	12.2	71.8	34	6	ABQ79034	Abq79034 Human Tcf
79	12.2	71.8	37	10	ACF58115	Acf58115 P14 targe
80	12.2	71.8	48	4	AAF84530	Aaf84530 Wheat tru
81	12.2	71.8	48	6	ADD41461	Add41461 Synthetic
82	12.2	71.8	50	4	AAL32180	Aal32180 Human SNP
83	12	70.6	20	2	AAT71200	Aat71200 Escherich
84	12	70.6	28	10	ADG76421	Adg76421 Primer #3
85	12	70.6	28	12	ADI21020	Adi21020 Citrate s
86	12	70.6	41	12	ADH05070	Adh05070 Gene poly
87	12	70.6	41	12	ADH05087	Adh05087 1-beta-me
88	11.8	69.4	17	2	AAV97452	Aav97452 Human EGF
89	11.8	69.4	18	2	AAV13291	Aav13291 Primer TP
90	11.8	69.4	18	6	ABK71978	Abk71978 Human MTG
91	11.8	69.4	19	11	ADL79445	Adl79445 Human HER
92	11.8	69.4	19	11	ADL79752	Adl79752 Human HER
93	11.8	69.4	20	3	AAC93241	Aac93241 Mouse STA



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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:41:56 ; Search time 590.305 Seconds  
(without alignments)  
1395.446 Million cell updates/sec

Title: US-10-712-882A-6  
Perfect score: 17  
Sequence: 1 tcctggttcgaggttaa 17

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : GenEmbl.\*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.in.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	6	A82478 Sequence 16
2	17	100.0	17	6	A84741 Sequence 2
3	17	100.0	17	6	AR144075 Sequence
4	17	100.0	17	6	BD246772 Diagnostic
5	17	100.0	17	6	BD271250 Predictio
6	17	100.0	17	6	I85579 Sequence 2
7	17	100.0	17	6	AR282878 Sequence
8	17	100.0	17	6	AR487086 Sequence
9	17	100.0	17	6	AR490514 Sequence
10	17	100.0	17	6	AR532947 Sequence
11	17	100.0	17	6	AR534189 Sequence
12	17	100.0	17	6	AX012494 Sequence
13	17	100.0	17	6	AX067287 Sequence
14	17	100.0	17	6	AX360018 Sequence
15	17	100.0	17	6	BD070853 Predictio
16	17	100.0	17	6	BD124539 Predictio
17	15.4	90.6	17	6	AR493815 Sequence
18	15.4	90.6	17	6	AX052798 Sequence
19	15.4	90.6	17	6	BD085842 Methods o

20	13	76.5	16	6	AR542778 Sequence
21	13	76.5	45	6	AR032344 Sequence
22	13	76.5	50	6	CQ008173 Sequence
23	12.8	75.3	24	6	AX268526 Sequence
24	12.8	75.3	27	6	AR116911 Sequence
25	12.8	75.3	27	6	AR182528 Sequence
26	12.8	75.3	47	6	AR289225 Sequence
27	12.8	75.3	48	6	AX426870 Sequence
28	12.8	75.3	50	6	CQ008796 Sequence
29	12.4	72.9	17	6	BD202865 Method an
30	12.4	72.9	22	6	AR483447 Sequence
31	12.4	72.9	22	6	BD089412 A method
32	12.4	72.9	22	12	AB068075 Synthetic
33	12.4	72.9	40	6	A99008 Sequence 16
34	12.4	72.9	40	6	A99009 Sequence 17
35	12.4	72.9	40	6	AR195325 Sequence
36	12.4	72.9	40	6	AR195326 Sequence
37	12.4	72.9	50	6	CQ005508 Sequence
38	12.2	71.8	19	6	AR026435 Sequence
39	12.2	71.8	19	6	AR070899 Sequence
40	12.2	71.8	19	6	AR143591 Sequence
41	12.2	71.8	19	6	AR143596 Sequence
42	12.2	71.8	20	6	AX295210 Sequence
43	12.2	71.8	24	6	AR268767 Sequence
44	12.2	71.8	24	6	AX290577 Sequence
45	12.2	71.8	29	6	CQ860037 Sequence
46	12.2	71.8	30	6	AR202722 Sequence
47	12.2	71.8	33	6	CQ860051 Sequence
48	12.2	71.8	48	6	AX113702 Sequence
49	12.2	71.8	50	6	CQ006748 Sequence
50	12	70.6	20	6	AR108128 Sequence
51	12	70.6	28	6	AX925901 Sequence
52	11.8	69.4	17	6	AR401892 Sequence
53	11.8	69.4	17	6	BD067392 Enzymatic
54	11.8	69.4	18	6	A67885 Sequence 57
55	11.8	69.4	20	6	AR121071 Sequence
56	11.8	69.4	20	6	AR130795 Sequence
57	11.8	69.4	20	6	BD272692 Antisense
58	11.8	69.4	20	6	AR531440 Sequence
59	11.8	69.4	20	6	BD089257 A method
60	11.8	69.4	20	12	AB067987 Synthetic
61	11.8	69.4	20	12	AB068032 Synthetic
62	11.8	69.4	20	12	ASJ10123 Artificial
63	11.8	69.4	21	6	AX451374 Sequence
64	11.8	69.4	21	6	AX553612 Sequence
65	11.8	69.4	21	6	AX613865 Sequence
66	11.8	69.4	21	6	BD088664 A method
67	11.8	69.4	21	12	AB067989 Synthetic
68	11.8	69.4	21	12	AB069355 Synthetic
69	11.8	69.4	24	6	E22929 Slit-like p
70	11.8	69.4	24	6	E26725 Vertebrate
71	11.8	69.4	25	6	CQ865161 Sequence
72	11.8	69.4	25	6	CQ865162 Sequence
73	11.8	69.4	27	6	AX278647 Sequence
74	11.8	69.4	30	6	AX937655 Sequence
75	11.8	69.4	31	6	CQ824301 Sequence
76	11.8	69.4	31	6	AX248869 Sequence
77	11.8	69.4	32	6	CQ824347 Sequence
78	11.8	69.4	32	6	AR274497 Sequence
79	11.8	69.4	36	6	AR007301 Sequence
80	11.8	69.4	39	9	AY082777 Homo sapi
81	11.8	69.4	47	6	AI0488 oligonucleo
82	11.8	69.4	47	6	AI3646 oligonucleo
83	11.8	69.4	47	6	AR288844 Sequence
84	11.8	69.4	48	6	I27649 Sequence 4
85	11.8	69.4	48	10	MMU12162 Mus musculu
86	11.8	69.4	48	10	M80442 Mouse T-cel
87	11.8	69.4	48	14	HIVF1Q5R5G Human immun
88	11.8	69.4	49	6	AR032437 Sequence
89	11.8	69.4	49	6	AR032438 Sequence
90	11.8	69.4	49	6	I29177 Sequence 49
91	11.8	69.4	49	6	I29178 Sequence 50
92	11.8	69.4	49	6	I90851 Sequence 49

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:30:35 ; Search time 260.181 Seconds  
(without alignments)  
455.077 Million cell updates/sec

Title: US-10-712-882A-5  
Perfect score: 17  
Sequence: 1 CTCGACCACTCTCAT 17

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 10399348

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/1/pubpna/US16\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	9	US-09-845-129-22
2	17	100.0	17	10	US-09-888-056A-3
3	17	100.0	17	15	US-10-167-127-23
4	17	100.0	17	16	US-10-172-919-7
5	17	100.0	17	16	US-10-320-360-1
6	17	100.0	17	19	US-10-802-061-22
7	17	100.0	17	20	US-10-823-197-7
8	17	100.0	17	22	Sequence 22, Appli
9	17	100.0	17	23	Sequence 23, Appli
10	17	100.0	17	24	Sequence 24, Appli
11	17	100.0	17	25	Sequence 25, Appli
12	17	100.0	17	26	Sequence 26, Appli
13	17	100.0	17	27	Sequence 27, Appli
14	17	100.0	17	28	Sequence 28, Appli
15	17	100.0	17	29	Sequence 29, Appli
16	17	100.0	17	30	Sequence 30, Appli
17	17	100.0	17	31	Sequence 31, Appli
18	17	100.0	17	32	Sequence 32, Appli
19	17	100.0	17	33	Sequence 33, Appli
20	17	100.0	17	34	Sequence 34, Appli
21	17	100.0	17	35	Sequence 35, Appli
22	17	100.0	17	36	Sequence 36, Appli
23	17	100.0	17	37	Sequence 37, Appli
24	17	100.0	17	38	Sequence 38, Appli
25	17	100.0	17	39	Sequence 39, Appli
26	17	100.0	17	40	Sequence 40, Appli
27	17	100.0	17	41	Sequence 41, Appli
28	17	100.0	17	42	Sequence 42, Appli
29	17	100.0	17	43	Sequence 43, Appli
30	17	100.0	17	44	Sequence 44, Appli
31	17	100.0	17	45	Sequence 45, Appli
32	17	100.0	17	46	Sequence 46, Appli
33	17	100.0	17	47	Sequence 47, Appli
34	17	100.0	17	48	Sequence 48, Appli
35	17	100.0	17	49	Sequence 49, Appli
36	17	100.0	17	50	Sequence 50, Appli
37	17	100.0	17	51	Sequence 51, Appli
38	17	100.0	17	52	Sequence 52, Appli
39	17	100.0	17	53	Sequence 53, Appli
40	17	100.0	17	54	Sequence 54, Appli
41	17	100.0	17	55	Sequence 55, Appli
42	17	100.0	17	56	Sequence 56, Appli
43	17	100.0	17	57	Sequence 57, Appli
44	17	100.0	17	58	Sequence 58, Appli
45	17	100.0	17	59	Sequence 59, Appli
46	17	100.0	17	60	Sequence 60, Appli
47	17	100.0	17	61	Sequence 61, Appli
48	17	100.0	17	62	Sequence 62, Appli
49	17	100.0	17	63	Sequence 63, Appli
50	17	100.0	17	64	Sequence 64, Appli
51	17	100.0	17	65	Sequence 65, Appli
52	17	100.0	17	66	Sequence 66, Appli
53	17	100.0	17	67	Sequence 67, Appli
54	17	100.0	17	68	Sequence 68, Appli
55	17	100.0	17	69	Sequence 69, Appli
56	17	100.0	17	70	Sequence 70, Appli
57	17	100.0	17	71	Sequence 71, Appli
58	17	100.0	17	72	Sequence 72, Appli
59	17	100.0	17	73	Sequence 73, Appli
60	17	100.0	17	74	Sequence 74, Appli
61	17	100.0	17	75	Sequence 75, Appli
62	17	100.0	17	76	Sequence 76, Appli
63	17	100.0	17	77	Sequence 77, Appli
64	17	100.0	17	78	Sequence 78, Appli
65	17	100.0	17	79	Sequence 79, Appli
66	17	100.0	17	80	Sequence 80, Appli
67	17	100.0	17	81	Sequence 81, Appli
68	17	100.0	17	82	Sequence 82, Appli
69	17	100.0	17	83	Sequence 83, Appli
70	17	100.0	17	84	Sequence 84, Appli
71	17	100.0	17	85	Sequence 85, Appli
72	17	100.0	17	86	Sequence 86, Appli
73	17	100.0	17	87	Sequence 87, Appli
74	17	100.0	17	88	Sequence 88, Appli
75	17	100.0	17	89	Sequence 89, Appli
76	17	100.0	17	90	Sequence 90, Appli
77	17	100.0	17	91	Sequence 91, Appli
78	17	100.0	17	92	Sequence 92, Appli
79	17	100.0	17	93	Sequence 93, Appli
80	17	100.0	17	94	Sequence 94, Appli
81	17	100.0	17	95	Sequence 95, Appli
82	17	100.0	17	96	Sequence 96, Appli
83	17	100.0	17	97	Sequence 97, Appli
84	17	100.0	17	98	Sequence 98, Appli
85	17	100.0	17	99	Sequence 99, Appli
86	17	100.0	17	100	Sequence 100, Appli

Sequence 5, Appli  
Sequence 9, Appli  
Sequence 504579,  
Sequence 936515,  
Sequence 9, Appli  
Sequence 422479,  
Sequence 201192,  
Sequence 505002,  
Sequence 707761,  
Sequence 88, Appli  
Sequence 88, Appli  
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Sequence 51845, A  
Sequence 51846, A  
Sequence 51850, A  
Sequence 51851, A  
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Sequence 491585,  
Sequence 71926,  
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Sequence 55182, A  
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Sequence 10841,  
Sequence 173875,  
Sequence 594385,  
Sequence 604072,  
Sequence 526931,  
Sequence 157655,  
Sequence 342430,  
Sequence 650876,  
Sequence 710320,  
Sequence 157, App  
Sequence 10897, A  
Sequence 10899, A  
Sequence 11041, A  
Sequence 11043, A  
Sequence 48043, A  
Sequence 48187, A  
Sequence 231135,  
Sequence 331110,  
Sequence 431922,  
Sequence 499674,  
Sequence 682363,  
Sequence 942483,  
Sequence 946235,  
Sequence 959361,  
Sequence 305219,  
Sequence 5674, Ap  
Sequence 6154, Ap  
Sequence 232023,  
Sequence 232503,  
Sequence 3467, Ap  
Sequence 29992, A  
Sequence 96575, A  
Sequence 12029, A  
Sequence 54143, A  
Sequence 312119,  
Sequence 578207,  
Sequence 108713,  
Sequence 665298,  
Sequence 699030,  
Sequence 750225,  
Sequence 751435,  
Sequence 131, App  
Sequence 131, App

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:11:51 ; Search time 41.6905 Seconds  
(without alignments)  
667.220 Million call updates/sec

Title: US-10-712-882A-5

Perfect score: 17

Sequence: 1 ctacgaacactcttat 17

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:\*

1: /cgm2\_6/ptodata/1/ina/5A COMB.seq:\*

2: /cgm2\_6/ptodata/1/ina/5B COMB.seq:\*

3: /cgm2\_6/ptodata/1/ina/6A COMB.seq:\*

4: /cgm2\_6/ptodata/1/ina/6B COMB.seq:\*

5: /cgm2\_6/ptodata/1/ina/PTCUS COMB.seq:\*

6: /cgm2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	1	US-08-628-282-1
2	17	100.0	17	2	US-08-587-911-1
3	17	100.0	17	3	US-08-813-456-1
4	17	100.0	17	3	US-09-345-217-22
5	17	100.0	17	4	US-09-431-352-1
6	17	100.0	17	4	US-09-845-129-22
7	17	100.0	17	4	US-09-037-472-5
8	17	100.0	17	4	US-09-578-534-7
9	17	100.0	17	4	US-09-632-657-9
10	17	100.0	17	4	US-09-693-555A-15
11	17	100.0	17	4	US-09-584-950-13
12	13.4	78.8	25	4	US-09-396-196G-117282
13	12.8	75.3	39	4	US-09-311-784A-131
14	12.4	72.9	25	1	US-08-375-116A-80
15	12.4	72.9	25	4	US-09-396-196G-9061
16	12.4	72.9	27	2	US-08-360-606B-19
17	12.4	72.9	29	4	US-09-304-233-299
18	12.2	71.8	20	1	US-08-063-167A-37
19	12.2	71.8	20	1	US-08-007-997A-37
20	12.2	71.8	20	2	US-08-440-740A-37
21	12.2	71.8	20	2	US-08-808-474A-27
22	12.2	71.8	20	2	US-08-344-155C-37
23	12.2	71.8	20	3	US-08-982-845B-37
24	12.2	71.8	20	3	US-08-991-525B-37
25	12.2	71.8	20	3	US-09-085-759-37
26	12.2	71.8	20	3	US-09-128-496-37
27	12.2	71.8	20	3	US-09-235-614-27
28	12.2	71.8	20	3	US-09-235-614-27
29	12.2	71.8	20	3	US-09-235-614-27
30	12.2	71.8	20	3	US-09-235-614-27
31	12.2	71.8	20	3	US-09-235-614-27
32	12.2	71.8	20	3	US-09-235-614-27
33	12.2	71.8	20	3	US-09-235-614-27
34	12.2	71.8	20	3	US-09-235-614-27
35	12.2	71.8	20	3	US-09-235-614-27
36	12.2	71.8	20	3	US-09-235-614-27
37	12.2	71.8	20	3	US-09-235-614-27
38	12.2	71.8	20	3	US-09-235-614-27
39	12.2	71.8	20	3	US-09-235-614-27
40	12.2	71.8	20	3	US-09-235-614-27
41	12.2	71.8	20	3	US-09-235-614-27
42	12.2	71.8	20	3	US-09-235-614-27
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44	12.2	71.8	20	3	US-09-235-614-27
45	12.2	71.8	20	3	US-09-235-614-27
46	12.2	71.8	20	3	US-09-235-614-27
47	12.2	71.8	20	3	US-09-235-614-27
48	12.2	71.8	20	3	US-09-235-614-27
49	12.2	71.8	20	3	US-09-235-614-27
50	12.2	71.8	20	3	US-09-235-614-27
51	12.2	71.8	20	3	US-09-235-614-27
52	12.2	71.8	20	3	US-09-235-614-27
53	12.2	71.8	20	3	US-09-235-614-27
54	12.2	71.8	20	3	US-09-235-614-27
55	12.2	71.8	20	3	US-09-235-614-27
56	12.2	71.8	20	3	US-09-235-614-27
57	12.2	71.8	20	3	US-09-235-614-27
58	12.2	71.8	20	3	US-09-235-614-27
59	12.2	71.8	20	3	US-09-235-614-27
60	12.2	71.8	20	3	US-09-235-614-27
61	12.2	71.8	20	3	US-09-235-614-27
62	12.2	71.8	20	3	US-09-235-614-27
63	12.2	71.8	20	3	US-09-235-614-27
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65	12.2	71.8	20	3	US-09-235-614-27
66	12.2	71.8	20	3	US-09-235-614-27
67	12.2	71.8	20	3	US-09-235-614-27
68	12.2	71.8	20	3	US-09-235-614-27
69	12.2	71.8	20	3	US-09-235-614-27
70	12.2	71.8	20	3	US-09-235-614-27
71	12.2	71.8	20	3	US-09-235-614-27
72	12.2	71.8	20	3	US-09-235-614-27
73	12.2	71.8	20	3	US-09-235-614-27
74	12.2	71.8	20	3	US-09-235-614-27
75	12.2	71.8	20	3	US-09-235-614-27
76	12.2	71.8	20	3	US-09-235-614-27
77	12.2	71.8	20	3	US-09-235-614-27
78	12.2	71.8	20	3	US-09-235-614-27
79	12.2	71.8	20	3	US-09-235-614-27
80	12.2	71.8	20	3	US-09-235-614-27
81	12.2	71.8	20	3	US-09-235-614-27
82	12.2	71.8	20	3	US-09-235-614-27
83	12.2	71.8	20	3	US-09-235-614-27
84	12.2	71.8	20	3	US-09-235-614-27
85	12.2	71.8	20	3	US-09-235-614-27
86	12.2	71.8	20	3	US-09-235-614-27
87	12.2	71.8	20	3	US-09-235-614-27
88	12.2	71.8	20	3	US-09-235-614-27
89	12.2	71.8	20	3	US-09-235-614-27
90	12.2	71.8	20	3	US-09-235-614-27
91	12.2	71.8	20	3	US-09-235-614-27
92	12.2	71.8	20	3	US-09-235-614-27
93	12.2	71.8	20	3	US-09-235-614-27
94	12.2	71.8	20	3	US-09-235-614-27
95	12.2	71.8	20	3	US-09-235-614-27
96	12.2	71.8	20	3	US-09-235-614-27
97	12.2	71.8	20	3	US-09-235-614-27
98	12.2	71.8	20	3	US-09-235-614-27
99	12.2	71.8	20	3	US-09-235-614-27
100	12.2	71.8	20	3	US-09-235-614-27

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Sequence 21, Appl  
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Sequence 21407, A  
Sequence 21420, A  
Sequence 82358, A  
Sequence 83359, A  
Sequence 117344, A  
Sequence 31, Appl  
Sequence 31, Appl  
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Sequence 67, Appl  
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Sequence 1532, Ap  
Sequence 1532, Ap  
Sequence 10043, A  
Sequence 7057, Ap  
Sequence 3433, Ap  
Sequence 3552, Ap  
Sequence 7111, Ap  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 51805, A  
Sequence 120134, A  
Sequence 14, Appl  
Sequence 4004, Ap  
Sequence 42, Appl  
Sequence 16, Appl  
Sequence 30, Appl  
Sequence 30, Appl  
Sequence 68, Appl  
Sequence 481, App  
Sequence 40852, A  
Sequence 51840, A  
Sequence 51841, A  
Sequence 51998, A  
Sequence 60446, A  
Sequence 84889, A  
Sequence 120385, A  
Sequence 120386, A  
Sequence 696, App  
Sequence 696, App  
Sequence 696, App  
Sequence 2298, Ap  
Sequence 2298, Ap  
Sequence 44, Appl  
Sequence 10361, A  
Sequence 13568, A  
Sequence 7275, Ap  
Sequence 44, Appl  
Sequence 38, Appl  
Sequence 23, Appl  
Sequence 36, Appl  
Sequence 40, Appl

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:46:26 ; Search time 1102.25 Seconds  
(without alignments)  
587.066 Million cell updates/sec

Title: US-10-712-882A-5  
Perfect score: 17  
Sequence: 1 ctacgaacactcttat 17

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : EST.\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	12.8	75.3	46	9	CR770256
c 2	12.8	75.3	47	8	BH855924
c 3	12.2	71.8	50	9	BX288701
c 4	12	70.6	36	8	AZ835422
c 5	12	70.6	44	8	BZ584309
c 6	11.8	69.4	32	4	BG391939
c 7	11.8	69.4	47	1	AA056223
c 8	11.8	69.4	50	1	AA103228
c 9	11.4	67.1	41	8	AZ777050
c 10	11.4	67.1	44	1	AJ795713
c 11	11.2	65.9	31	9	AL938736
c 12	11.2	65.9	34	8	BZ358990
c 13	11.2	65.9	36	9	CL640799
c 14	11.2	65.9	38	8	AZ810473
c 15	11.2	65.9	42	9	CL437514
c 16	11.2	65.9	43	8	AZ336476
c 17	11.2	65.9	44	1	AA968783
c 18	11.2	65.9	47	1	AA570265
c 19	11.2	65.9	47	8	BZ663174
c 20	11.2	65.9	49	1	AJ136193
c 21	11.2	65.9	50	1	AJ106610
c 22	11.2	65.9	50	9	AG202430
c 23	11	64.7	39	8	AZ588494
c 24	11	64.7	46	8	AZ507219

25	10.8	63.5	25	8	AZ588797	1M0397D21
26	10.8	63.5	26	8	AZ587584	1M0395C23
27	10.8	63.5	28	8	AQ073689	BP(2)2563
c 28	10.8	63.5	31	1	AA847844	cd39a01.8
c 29	10.8	63.5	34	1	AA912187	cd121d04.8
c 30	10.8	63.5	38	8	AZ447531	1M0244C15
31	10.8	63.5	40	1	AU260045	AU260045
32	10.8	63.5	41	9	DMES46454	DMES46454
c 33	10.8	63.5	43	1	AA171959	AA171959
c 34	10.8	63.5	43	8	AZ304932	1M0005G03
c 35	10.8	63.5	45	8	AZ411401	1M0184M20
c 36	10.8	63.5	47	1	AJ721362	AJ721362
c 37	10.8	63.5	49	1	AI218813	AI218813
c 38	10.8	63.5	50	1	AU103366	AU103366
39	10.6	62.4	28	8	AZ477874	1M0297O22
40	10.6	62.4	29	9	AG194367	Pan trogl
41	10.6	62.4	34	8	AZ646197	AZ646197
c 42	10.6	62.4	37	9	TA115G06P	TA115G06P
c 43	10.6	62.4	40	8	CC456164	CC456164
c 44	10.6	62.4	40	9	CC794012	CC794012
c 45	10.6	62.4	40	9	CC885461	CC885461
c 46	10.6	62.4	42	8	AZ437308	1M0275D05
c 47	10.6	62.4	42	9	DMES47250	DMES47250
c 48	10.6	62.4	43	1	AI910779	AI910779
50	10.6	62.4	46	8	CC178564	CC178564
51	10.6	62.4	46	9	CG672156	CG672156
52	10.6	62.4	47	8	AZ799594	2M0057H09
53	10.6	62.4	47	8	BH624301	1M0710SH0
54	10.6	62.4	49	8	BZ380372	BZ380372
55	10.6	62.4	49	9	CR397086	CR397086
56	10.6	62.4	50	1	AU105021	AU105021
57	10.6	62.4	50	1	AU105022	AU105022
58	10.6	62.4	50	1	AU105025	AU105025
59	10.6	62.4	50	1	AU105033	AU105033
60	10.6	62.4	50	1	AU105037	AU105037
61	10.6	62.4	50	1	AU105047	AU105047
62	10.6	62.4	50	1	AU105075	AU105075
63	10.6	62.4	50	1	AU105089	AU105089
64	10.6	62.4	50	1	AU105093	AU105093
65	10.6	62.4	50	1	AU106939	AU106939
c 66	10.6	62.4	50	8	AZ817325	2M0086C23
c 67	10.6	62.4	50	8	BH905738	SALK 1076
c 68	10.4	61.2	21	8	AZ308559	1M0011J09
69	10.4	61.2	22	8	AZ472622	1M0287N20
c 70	10.4	61.2	22	8	AZ761328	1M0555A11
c 71	10.4	61.2	30	9	AL936083	Arabidops
c 72	10.4	61.2	31	7	CF291233	14ROOR--0
c 73	10.4	61.2	31	8	AZ615738	1M0445A14
c 74	10.4	61.2	36	8	AZ603547	1M0422O21
75	10.4	61.2	37	8	AZ474017	1M0290A18
c 76	10.4	61.2	39	1	AA911358	oe76d10.8
c 77	10.4	61.2	39	8	AZ424411	1M0204F04
c 78	10.4	61.2	39	9	TA110A12Q	TA110A12Q
79	10.4	61.2	40	1	AA434732	AA434732
80	10.4	61.2	42	9	AG204495	Pan trogl
81	10.4	61.2	43	9	AL944653	Arabidops
82	10.4	61.2	45	4	BJ015280	BJ015280
c 83	10.4	61.2	47	1	AA486931	ab17b11.r
84	10.4	61.2	49	1	AI385645	md74c04.x
85	10.4	61.2	50	1	AU103566	AU103566
c 86	10.4	61.2	50	4	BG271838	na154f12
87	10.4	61.2	50	5	BP133040	BP133040
88	10.4	61.2	50	5	BQ613522	rd08f05.y
c 89	10.2	60.0	20	8	AZ830285	2M0109N22
90	10.2	60.0	21	7	CO791110	NT011C.A0
91	10.2	60.0	22	8	AZ312656	1M0028J14
c 92	10.2	60.0	25	9	AJ590349	Arabidops
93	10.2	60.0	31	1	AA511446	v127h04.r
94	10.2	60.0	31	8	BH861784	SALK 0879
c 95	10.2	60.0	32	6	CD534045	35C5_Arab
96	10.2	60.0	34	8	AZ775415	2M0007M16
c 97	10.2	60.0	34	8	BH849503	SALK_0697

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 16:54:30 ; Search time 147.09 Seconds  
(without alignments)  
684.175 Million cell updates/sec

Title: US-10-712-882A-5

Perfect score: 17

Sequence: 1 ctcagcaaacactctat 17

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : N Geneseq 16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	17	100.0	17	2	AAT89947 Human Int
2	17	100.0	17	2	AAT89409 Human IL-
3	17	100.0	17	2	AAV62390 IL-1 rece
4	17	100.0	17	2	AAV60230 PCR prime
5	17	100.0	17	2	AAV32393 Interleuk
6	17	100.0	17	2	AAZ10706 PCR prime
7	17	100.0	17	2	AAZ10706 PCR prime
8	17	100.0	17	2	AAZ10706 PCR prime
9	17	100.0	17	2	AAZ10706 PCR prime
10	17	100.0	17	2	AAZ10706 PCR prime
11	17	100.0	17	3	AAZ15549 Human IL-
12	17	100.0	17	3	AAZ15549 Human IL-
13	17	100.0	17	3	AAZ15549 Human IL-
14	17	100.0	17	3	AAZ15549 Human IL-
15	17	100.0	17	5	AAZ15549 Human IL-
16	17	100.0	17	5	AAZ15549 Human IL-
17	17	100.0	17	6	AAZ15549 Human IL-
18	17	100.0	17	8	AAZ15549 Human IL-
19	17	100.0	17	10	AAZ15549 Human IL-
20	17	100.0	17	12	AAZ15549 Human IL-

17	100.0	17	12	ADO35276	Ado35276 Human int
21	82.4	17	8	ACC44794	Acc44794 Interleuk
22	81.2	20	10	ACA58140	Acc58140 Human fam
23	13.8	19	4	AAH20018	Aah20018 Mouse PAF
24	13	50	6	ABZ00166	Abz00166 Human leu
25	76.5	50	12	ADP10101	Adp10101 50-mer ol
26	13	39	3	AAZ46209	Aaz46209 PMIN 1-Sw
27	75.3	42	12	ADN36372	Adn36372 Bacillus
28	75.3	16	10	ADN36372	Adn36372 PCR prime
29	72.9	17	6	ACN01682	Acn01682 WNV Inozy
30	72.9	17	6	ACN01683	Acn01683 WNV Inozy
31	72.9	17	6	ACN00198	Acn00198 WNV Hamme
32	72.9	17	6	ACN14095	Acn14095 WNV minus
33	72.9	17	6	ACN15151	Acn15151 WNV minus
34	72.9	20	12	ADH44459	Adh44459 Human RB2
35	72.9	20	12	ADH44459	Adh44459 Human RB2
36	72.9	24	6	AAAL40477	Aal40477 PAAD doma
37	72.9	24	6	AAAL40472	Aal40472 PAAD doma
38	72.9	24	6	AAAL40472	Aal40472 PAAD doma
39	72.9	24	6	AAAL40472	Aal40472 PAAD doma
40	72.9	24	6	AAAL40472	Aal40472 PAAD doma
41	72.9	24	6	AAAL40472	Aal40472 PAAD doma
42	72.9	24	6	AAAL40472	Aal40472 PAAD doma
43	72.9	24	6	AAAL40472	Aal40472 PAAD doma
44	72.9	24	6	AAAL40472	Aal40472 PAAD doma
45	72.9	24	6	AAAL40472	Aal40472 PAAD doma
46	72.9	24	6	AAAL40472	Aal40472 PAAD doma
47	72.9	24	6	AAAL40472	Aal40472 PAAD doma
48	72.9	24	6	AAAL40472	Aal40472 PAAD doma
49	72.9	24	6	AAAL40472	Aal40472 PAAD doma
50	72.9	24	6	AAAL40472	Aal40472 PAAD doma
51	72.9	24	6	AAAL40472	Aal40472 PAAD doma
52	72.9	24	6	AAAL40472	Aal40472 PAAD doma
53	72.9	24	6	AAAL40472	Aal40472 PAAD doma
54	72.9	24	6	AAAL40472	Aal40472 PAAD doma
55	72.9	24	6	AAAL40472	Aal40472 PAAD doma
56	72.9	24	6	AAAL40472	Aal40472 PAAD doma
57	72.9	24	6	AAAL40472	Aal40472 PAAD doma
58	72.9	24	6	AAAL40472	Aal40472 PAAD doma
59	72.9	24	6	AAAL40472	Aal40472 PAAD doma
60	72.9	24	6	AAAL40472	Aal40472 PAAD doma
61	72.9	24	6	AAAL40472	Aal40472 PAAD doma
62	72.9	24	6	AAAL40472	Aal40472 PAAD doma
63	72.9	24	6	AAAL40472	Aal40472 PAAD doma
64	72.9	24	6	AAAL40472	Aal40472 PAAD doma
65	72.9	24	6	AAAL40472	Aal40472 PAAD doma
66	72.9	24	6	AAAL40472	Aal40472 PAAD doma
67	72.9	24	6	AAAL40472	Aal40472 PAAD doma
68	72.9	24	6	AAAL40472	Aal40472 PAAD doma
69	72.9	24	6	AAAL40472	Aal40472 PAAD doma
70	72.9	24	6	AAAL40472	Aal40472 PAAD doma
71	72.9	24	6	AAAL40472	Aal40472 PAAD doma
72	72.9	24	6	AAAL40472	Aal40472 PAAD doma
73	72.9	24	6	AAAL40472	Aal40472 PAAD doma
74	72.9	24	6	AAAL40472	Aal40472 PAAD doma
75	72.9	24	6	AAAL40472	Aal40472 PAAD doma
76	72.9	24	6	AAAL40472	Aal40472 PAAD doma
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81	72.9	24	6	AAAL40472	Aal40472 PAAD doma
82	72.9	24	6	AAAL40472	Aal40472 PAAD doma
83	72.9	24	6	AAAL40472	Aal40472 PAAD doma
84	72.9	24	6	AAAL40472	Aal40472 PAAD doma
85	72.9	24	6	AAAL40472	Aal40472 PAAD doma
86	72.9	24	6	AAAL40472	Aal40472 PAAD doma
87	72.9	24	6	AAAL40472	Aal40472 PAAD doma
88	72.9	24	6	AAAL40472	Aal40472 PAAD doma
89	72.9	24	6	AAAL40472	Aal40472 PAAD doma
90	72.9	24	6	AAAL40472	Aal40472 PAAD doma
91	72.9	24	6	AAAL40472	Aal40472 PAAD doma
92	72.9	24	6	AAAL40472	Aal40472 PAAD doma
93	72.9	24	6	AAAL40472	Aal40472 PAAD doma

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:41:56 ; Search time 590.305 Seconds  
(without alignments)  
1395.446 Million cell updates/sec

Title: US-10-712-882A-5

Perfect score: 17

Sequence: 1 ctcagcaacactccat 17

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	6	A82477 Sequence 15
2	17	100.0	17	6	A84740 Sequence 1
3	17	100.0	17	6	AR144074 Sequence
4	17	100.0	17	6	BD246771
5	17	100.0	17	6	BD271249
6	17	100.0	17	6	BD271249 Diagnosti
7	17	100.0	17	6	I85578 Sequence 1
8	17	100.0	17	6	AR282877 Sequence
9	17	100.0	17	6	AR487085 Sequence
10	17	100.0	17	6	AR490513 Sequence
11	17	100.0	17	6	AR493814 Sequence
12	17	100.0	17	6	AR532946 Sequence
13	17	100.0	17	6	AR534188 Sequence
14	17	100.0	17	6	AR542777 Sequence
15	17	100.0	17	6	AX012493 Sequence
16	17	100.0	17	6	AX052797 Sequence
17	17	100.0	17	6	AX067286 Sequence
18	17	100.0	17	6	AX360017 Sequence
19	17	100.0	17	6	BD070852 Predictio
					BD085841 Methods o

20	17	100.0	17	6	BD124538
21	14.4	84.7	45	5	GGOVO2
22	13	76.5	19	6	AX113043
23	12.8	75.3	39	6	BD238569
24	12.4	72.9	24	6	AX417233
25	12.4	72.9	24	6	AX417233 Sequence
26	12.4	72.9	25	6	I43262
27	12.2	71.8	20	6	AR026564
28	12.2	71.8	20	6	AR062637
29	12.2	71.8	20	6	AR104740
30	12.2	71.8	20	6	AR105562
31	12.2	71.8	20	6	AR123324
32	12.2	71.8	20	6	AR129012
33	12.2	71.8	20	6	I20639
34	12.2	71.8	20	6	I33332
35	12.2	71.8	20	6	AR312142
36	12.2	71.8	20	6	AR370562
37	12.2	71.8	21	6	AR067354
38	12.2	71.8	21	6	AR122750
39	12.2	71.8	21	6	BD103554
40	12.2	71.8	23	6	BD170001
41	12.2	71.8	29	6	CQ770408
42	12.2	71.8	29	6	CQ770411
43	12.2	71.8	43	6	AX787113
44	12.2	71.8	45	9	HUMPAIB9
45	12	70.6	20	6	AR262282
46	12	70.6	20	6	AR262283
47	12	70.6	20	6	AX402174
48	12	70.6	24	6	AX444158
49	12	70.6	25	6	AX448125
50	11.8	69.4	18	6	AR045242
51	11.8	69.4	18	6	I52294
52	11.8	69.4	20	6	AR295023
53	11.8	69.4	20	6	AR312127
54	11.8	69.4	20	6	AR312134
55	11.8	69.4	25	6	I43275
56	11.8	69.4	31	6	AX248139
57	11.8	69.4	32	6	AR139786
58	11.8	69.4	32	6	AR174609
59	11.8	69.4	32	6	BD249002
60	11.8	69.4	32	6	AR208464
61	11.8	69.4	32	6	AR279248
62	11.8	69.4	32	6	AR339843
63	11.8	69.4	32	6	AR374101
64	11.8	69.4	32	6	AR456251
65	11.8	69.4	32	6	BD086232
66	11.8	69.4	33	6	E04332
67	11.8	69.4	36	6	AR174646
68	11.8	69.4	36	6	BD249039
69	11.8	69.4	36	6	AR374138
70	11.8	69.4	36	6	AR456288
71	11.8	69.4	38	6	AR046739
72	11.8	69.4	38	6	I53791
73	11.8	69.4	38	6	AR332641
74	11.8	69.4	38	6	AX581051
75	11.8	69.4	39	6	E14084
76	11.8	69.4	41	6	AX515021
77	11.8	69.4	41	6	AX519221
78	11.8	69.4	45	6	AX460809
79	11.8	69.4	47	6	AR291698
80	11.8	69.4	47	6	AR291817
81	11.6	68.2	46	6	AX357203
82	11.4	67.1	20	6	BD141098
83	11.4	67.1	20	6	AX294987
84	11.4	67.1	21	6	CQ830925
85	11.4	67.1	21	6	AR295376
86	11.4	67.1	21	6	AR329076
87	11.4	67.1	22	6	AR372093
88	11.4	67.1	22	6	AX535285
89	11.4	67.1	24	6	AX290354
90	11.4	67.1	24	6	AX443723
91	11.4	67.1	24	6	AX447439
92	11.4	67.1	25	6	AX447704

BD124538	Predictio
V00441	Chicken ovo
AX113043	Sequence
BD238569	Expressio
AX417233	Sequence
AX417238	Sequence
I43262	Sequence 80
AR026564	Sequence
AR062637	Sequence
AR104740	Sequence
AR105562	Sequence
AR123324	Sequence
AR129012	Sequence
I20639	Sequence 37
I33332	Sequence 37
AR312142	Sequence
AR370562	Sequence
AR067354	Sequence
AR122750	Sequence
BD103554	Saccharid
BD170001	Novel pro
CQ770408	Sequence
CQ770411	Sequence
AX787113	Sequence
M22321	Human plasm
AR262282	Sequence
AR262283	Sequence
AX402174	Sequence
AX444158	Sequence
AX448125	Sequence
AR045242	Sequence
I52294	Sequence 35
AR295023	Sequence
AR312127	Sequence
AR312134	Sequence
I43275	Sequence 93
AX248139	Sequence
AR139786	Sequence
AR174609	Sequence
BD249002	Novel cyt
AR208464	Sequence
AR279248	Sequence
AR339843	Sequence
AR374101	Sequence
AR456251	Sequence
BD086232	Transcrip
E04332	Primer for
AR174646	Sequence
BD249039	Novel cyt
AR374138	Sequence
AR456288	Sequence
AR046739	Sequence
I53791	Sequence 15
AR332641	Sequence
AX581051	Sequence
E14084	Primer, 7/1
AX515021	Sequence
AX519221	Sequence
AX460809	Sequence
AR291698	Sequence
AR291817	Sequence
AX357203	Sequence
BD141098	A highly
AX294987	Sequence
CQ830925	Sequence
AR295376	Sequence
AR329076	Sequence
AR372093	Sequence
AX535285	Sequence
AX290354	Sequence
AX443723	Sequence
AX447439	Sequence
AX447704	Sequence

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:30:35 ; Search time 306.095 Seconds  
(without alignments)  
455.077 Million cell updates/sec

Title: US-10-712-882A-4

Perfect score: 20

Sequence: 1 gtttaggaattctccactt 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 10399348

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	9	US-09-852-948-2
2	20	100.0	20	9	US-09-845-129-17
3	20	100.0	20	10	US-09-950-935-15
4	20	100.0	20	10	US-09-888-056A-10
5	20	100.0	20	13	US-10-032-242A-2
6	20	100.0	20	15	US-10-167-127-20
7	20	100.0	20	16	US-10-172-919-29
Sequence 2, Appli					
Sequence 17, Appli					
Sequence 15, Appli					
Sequence 10, Appli					
Sequence 20, Appli					
Sequence 29, Appli					

20	100.0	20	16	US-10-320-360-6	Sequence 6, Appli
20	100.0	20	19	US-10-802-061-17	Sequence 17, Appli
20	100.0	20	20	US-10-626-830-8	Sequence 8, Appli
20	100.0	20	20	US-10-823-197-4	Sequence 4, Appli
20	100.0	20	21	US-10-712-882-4	Sequence 4, Appli
20	100.0	20	21	US-10-838-503-18	Sequence 18, Appli
20	100.0	20	21	US-10-719-900-217359	Sequence 217359,
25	15.8	79.0	25	US-10-719-900-569772	Sequence 569772,
15	15.4	77.0	25	US-10-719-956-688359	Sequence 688359,
16	15	75.0	25	US-10-476-264-234	Sequence 234, App
17	14.8	74.0	25	US-10-719-956-543394	Sequence 543394,
18	14.8	74.0	25	US-10-719-900-822565	Sequence 822565,
19	14.4	72.0	25	US-10-719-956-293010	Sequence 293010,
20	14.4	72.0	25	US-10-719-900-822565	Sequence 822565,
21	14.4	72.0	25	US-11-036-317-491552	Sequence 491552,
22	14.4	72.0	25	US-11-036-317-501217	Sequence 501217,
23	14.4	72.0	25	US-11-036-317-532740	Sequence 532740,
24	14.4	72.0	25	US-11-036-317-532741	Sequence 532741,
25	14.4	72.0	25	US-11-036-317-569906	Sequence 569906,
26	14.4	72.0	25	US-11-036-317-562013	Sequence 562013,
27	14.4	72.0	25	US-11-036-317-643222	Sequence 643222,
28	14.2	71.0	25	US-10-098-263B-67944	Sequence 67944, A
29	14.2	71.0	25	US-10-719-900-217360	Sequence 217360,
30	14.2	71.0	25	US-10-719-900-812651	Sequence 812651,
31	14.2	71.0	25	US-10-719-900-82652	Sequence 82652,
32	14.2	71.0	25	US-10-719-900-884140	Sequence 884140,
33	14.2	71.0	25	US-10-719-900-971261	Sequence 971261,
34	14.2	71.0	25	US-10-719-956-374195	Sequence 374195,
35	14	70.0	25	US-10-956-157-276008	Sequence 276008,
36	14	70.0	48	US-10-131-827-862	Sequence 862, App
37	13.8	69.0	25	US-10-719-900-109428	Sequence 109428,
38	13.8	69.0	25	US-10-719-900-133074	Sequence 133074,
39	13.8	69.0	25	US-10-719-900-133814	Sequence 133814,
40	13.8	69.0	25	US-10-719-900-410237	Sequence 410237,
41	13.8	69.0	25	US-10-719-900-569773	Sequence 569773,
42	13.8	69.0	25	US-10-719-900-747446	Sequence 747446,
43	13.8	69.0	25	US-10-719-900-886201	Sequence 886201,
44	13.8	69.0	25	US-10-719-900-886202	Sequence 886202,
45	13.8	69.0	25	US-10-956-157-281192	Sequence 281192,
46	13.8	69.0	25	US-10-719-956-480144	Sequence 480144,
47	13.8	69.0	25	US-11-036-317-148591	Sequence 148591,
48	13.8	69.0	25	US-11-036-317-181201	Sequence 181201,
49	13.8	69.0	25	US-11-036-317-261570	Sequence 261570,
50	13.8	69.0	25	US-11-036-317-290923	Sequence 290923,
51	13.8	69.0	25	US-11-036-317-321592	Sequence 321592,
52	13.8	69.0	25	US-11-036-317-820539	Sequence 820539,
53	13.8	69.0	42	US-10-263-103-2	Sequence 2, Appli
54	13.8	69.0	42	US-10-263-103-3	Sequence 3, Appli
55	13.8	69.0	48	US-10-179-152-8	Sequence 8, Appli
56	13.6	68.0	25	US-10-215-112-5672	Sequence 5672, Ap
57	13.6	68.0	25	US-10-719-900-586840	Sequence 586840,
58	13.6	68.0	25	US-10-719-900-741504	Sequence 741504,
59	13.6	68.0	25	US-10-719-900-790357	Sequence 790357,
60	13.6	68.0	25	US-10-719-900-790939	Sequence 790939,
61	13.6	68.0	25	US-10-719-900-911166	Sequence 911166,
62	13.6	68.0	25	US-10-719-956-142021	Sequence 142021,
63	13.6	68.0	25	US-10-719-956-350887	Sequence 350887,
64	13.4	67.0	19	US-09-969-373-1558	Sequence 1558, Ap
65	13.4	67.0	25	US-10-719-956-124722	Sequence 124722,
66	13.4	67.0	25	US-10-719-956-597269	Sequence 597269,
67	13.4	67.0	25	US-10-719-956-688360	Sequence 688360,
68	13.4	67.0	25	US-11-036-317-179602	Sequence 179602,
69	13.4	67.0	25	US-11-036-317-253691	Sequence 253691,
70	13.4	67.0	25	US-11-036-317-277420	Sequence 277420,
71	13.4	67.0	25	US-11-036-317-384247	Sequence 384247,
72	13.4	67.0	25	US-11-036-317-548104	Sequence 548104,
73	13.4	67.0	25	US-11-036-317-751492	Sequence 751492,
74	13.4	67.0	25	US-11-036-317-820523	Sequence 820523,
75	13.4	67.0	25	US-11-036-317-865407	Sequence 865407,
76	13.4	67.0	25	US-11-036-317-907498	Sequence 907498,
77	13.4	67.0	25	US-11-036-317-907723	Sequence 907723,
78	13.4	67.0	25	US-11-036-317-969789	Sequence 969789,
79	13.4	67.0	25	US-11-036-317-982716	Sequence 982716,
80	13.2	66.0	20	US-10-473-368-2	Sequence 2, Appli

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:11:51 ; Search time 49.0476 Seconds  
(without alignments)  
667.220 Million cell updates/sec

Title: US-10-712-882A-4

Perfect score: 20

Sequence: 1 gtttaggaattccactt 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:  
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5: /cgm2\_6/ptodata/1/ina/PCTUS COMB.seq:  
6: /cgm2\_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	US-08-510-696-4
2	20	100.0	20	3	US-09-005-923-4
3	20	100.0	20	3	US-08-813-456-4
4	20	100.0	20	3	US-09-183-850-2
5	20	100.0	20	3	US-09-345-117-17
6	20	100.0	20	4	US-09-431-352-6
7	20	100.0	20	4	US-09-852-948-2
8	20	100.0	20	4	US-09-845-129-17
9	20	100.0	20	4	US-09-037-472-4
10	20	100.0	20	4	US-09-578-534-4
11	20	100.0	20	4	US-09-632-557-18
12	20	100.0	20	4	US-09-693-555A-4
13	20	100.0	20	4	US-09-584-950-12
14	20	100.0	20	5	PCT-US96-12455-4
15	14.2	71.0	25	1	US-08-599-252-62
16	14.2	71.0	25	5	PCT-US96-06352-62
17	14.2	71.0	25	5	PCT-US96-06583-62
18	14.2	71.0	27	1	US-07-977-284A-186
19	14.2	71.0	27	2	US-08-256-426B-186
20	13.8	69.0	42	4	US-10-263-103-3
21	13.8	69.0	42	4	US-10-263-103-3
22	13.8	69.0	48	4	US-09-164-880A-8
23	13.2	66.0	47	4	US-09-422-978-334
24	13	65.0	20	4	US-09-198-452A-1701
25	12.8	64.0	22	3	US-08-974-549A-526
26	12.8	64.0	22	4	US-08-912-951-293
27	12.8	64.0	22	4	US-09-402-181B-526

28	12.8	64.0	22	4	US-09-721-456-526	Sequence 526, App
29	12.6	63.0	20	3	US-09-280-805-217	Sequence 217, App
30	12.6	63.0	24	1	US-07-722-798A-45	Sequence 45, Appl
31	12.6	63.0	24	3	US-08-943-731-228	Sequence 228, App
32	12.6	63.0	29	3	US-08-181-664-14	Sequence 14, Appl
33	12.6	63.0	29	4	US-08-825-746-15	Sequence 15, Appl
34	12.4	62.0	25	4	US-09-396-196G-6497	Sequence 6497, Ap
35	12.4	62.0	25	4	US-09-396-196G-6498	Sequence 6498, Ap
36	12.4	62.0	25	4	US-09-396-196G-6499	Sequence 6499, Ap
37	12.4	62.0	25	4	US-09-396-196G-27362	Sequence 27362, A
38	12.2	61.0	20	3	US-08-949-344C-15	Sequence 15, Appl
39	12.2	61.0	21	3	US-09-363-316B-19	Sequence 19, Appl
40	12.2	61.0	21	4	US-10-136-227A-19	Sequence 19, Appl
41	12.2	61.0	21	4	US-09-981-649A-19	Sequence 19, Appl
42	12.2	61.0	25	4	US-09-396-196G-37868	Sequence 37868, A
43	12.2	61.0	25	4	US-09-396-196G-78637	Sequence 78637, A
44	12.2	61.0	25	4	US-09-396-196G-95876	Sequence 95876, A
45	12.2	61.0	26	3	US-09-245-041-100	Sequence 100, App
46	12.2	61.0	26	4	US-09-358-058B-101	Sequence 101, App
47	12.2	61.0	26	4	US-09-893-238-100	Sequence 100, App
48	12.2	61.0	37	1	US-08-468-700-14	Sequence 14, Appl
49	12.2	61.0	37	2	US-08-704-706A-14	Sequence 14, Appl
50	12.2	61.0	37	3	US-08-985-659-14	Sequence 14, Appl
51	12.2	61.0	39	3	US-09-082-649B-47	Sequence 47, Appl
52	12.2	61.0	39	4	US-10-327-189-21	Sequence 21, Appl
53	12.2	61.0	39	4	US-10-327-189-22	Sequence 22, Appl
54	12.2	61.0	39	4	US-09-965-101-47	Sequence 47, Appl
55	12.2	61.0	40	2	US-08-768-964-10	Sequence 10, Appl
56	12.2	61.0	40	3	US-09-005-299-10	Sequence 10, Appl
57	12.2	61.0	40	3	US-09-515-431-10	Sequence 10, Appl
58	12.2	61.0	47	4	US-09-422-978-2936	Sequence 2936, Ap
59	12.2	61.0	49	2	US-08-850-049-56	Sequence 56, Appl
60	12.2	61.0	49	2	US-08-050-478-56	Sequence 56, Appl
61	12.2	61.0	49	3	US-09-414-117-56	Sequence 56, Appl
62	12.2	61.0	49	3	US-09-678-437-56	Sequence 56, Appl
63	12.2	61.0	49	4	US-09-943-722-56	Sequence 56, Appl
64	12	60.0	39	4	US-09-644-987-3	Sequence 3, Appl
65	12	60.0	42	4	US-09-043-861-21	Sequence 21, Appl
66	12	60.0	47	4	US-09-422-978-221	Sequence 221, App
67	12	60.0	49	4	US-09-378-847-16	Sequence 16, Appl
68	12	60.0	49	4	US-09-378-810-16	Sequence 16, Appl
69	11.8	59.0	17	1	US-08-388-381-37	Sequence 37, Appl
70	11.8	59.0	17	3	US-08-765-626-37	Sequence 37, Appl
71	11.8	59.0	17	5	PCT-US95-08605-37	Sequence 37, Appl
72	11.8	59.0	20	3	US-08-854-170-5	Sequence 5, Appl
73	11.8	59.0	20	3	US-08-181-664-6	Sequence 65, Appl
74	11.8	59.0	21	4	US-09-520-781-65	Sequence 35, Appl
75	11.8	59.0	22	3	US-09-288-339-35	Sequence 35, Appl
76	11.8	59.0	25	4	US-09-396-196G-95875	Sequence 95875, A
77	11.8	59.0	25	4	US-09-396-196G-127105	Sequence 127105, A
78	11.8	59.0	28	1	US-08-233-597-8	Sequence 8, Appl
79	11.8	59.0	30	2	US-08-418-848A-20	Sequence 20, Appl
80	11.8	59.0	32	3	US-08-181-664-77	Sequence 77, Appl
81	11.8	59.0	36	4	US-09-826-509-32	Sequence 32, Appl
82	11.8	59.0	37	1	US-08-468-700-18	Sequence 18, Appl
83	11.8	59.0	37	1	US-08-468-700-21	Sequence 21, Appl
84	11.8	59.0	37	2	US-08-704-706A-18	Sequence 18, Appl
85	11.8	59.0	37	2	US-08-704-706A-21	Sequence 21, Appl
86	11.8	59.0	37	3	US-08-985-659-18	Sequence 18, Appl
87	11.8	59.0	37	3	US-08-985-659-21	Sequence 21, Appl
88	11.8	59.0	41	3	US-08-813-507-76	Sequence 76, Appl
89	11.8	59.0	41	3	US-09-464-453-76	Sequence 76, Appl
90	11.6	58.0	24	2	US-08-332-766A-105	Sequence 105, App
91	11.6	58.0	25	3	US-08-814-413-19	Sequence 19, Appl
92	11.6	58.0	25	4	US-09-396-196G-25403	Sequence 25403, A
93	11.6	58.0	25	4	US-09-396-196G-25414	Sequence 25414, A
94	11.6	58.0	27	1	US-08-640-517A-39	Sequence 39, Appl
95	11.6	58.0	27	2	US-08-874-678-24	Sequence 24, Appl
96	11.6	58.0	27	3	US-08-643-839-24	Sequence 24, Appl
97	11.6	58.0	27	3	US-09-348-886-24	Sequence 24, Appl
98	11.6	58.0	29	2	US-08-859-998-416	Sequence 416, App
99	11.6	58.0	29	3	US-09-225-928-416	Sequence 416, App
100	11.6	58.0	29	4	US-09-225-201B-416	Sequence 416, App



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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:46:26 ; Search time 1296.76 Seconds  
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587.066 Million cell updates/sec

Title: US-10-712-882A-4

Perfect score: 20  
Sequence: 1 gtttaggaattccactt 20

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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- 2: gb\_est2.\*
- 3: gb\_hic.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_gse1.\*
- 9: gb\_gse2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.2	71.0	43	1	AA101435 zn72904.r
2	13.6	68.0	42	9	CR404914 Arabidops
3	12.8	64.0	19	9	AJ588791 Arabidops
4	12.6	63.0	30	8	AZ437578 IM0225124
5	12.6	63.0	35	8	AZ345589 IM0080N16
6	12.6	63.0	39	8	BH49007 SALK_0691
7	12.6	63.0	39	9	AJ587663 Arabidops
8	12.6	63.0	44	8	BZ356349 SALK_1288
9	12.6	63.0	46	8	BZ663309 SALK_0269
10	12.6	63.0	49	9	AL769017 Arabidops
11	12.4	62.0	42	9	AL937418 Arabidops
12	12.2	61.0	36	7	CF973738 FSU_Joea
13	12.2	61.0	38	8	AZ602389 IM0421D10
14	12.2	61.0	42	9	BX892496 Arabidops
15	12.2	61.0	50	1	AU103941 Arabidops
16	12.2	61.0	35	8	BZ354715 SALK_1256
17	12.2	60.0	39	8	AZ839400 2M0135E06
18	12.2	60.0	40	9	CG714954 1119039C0
19	12.2	60.0	42	8	BH903125 SALK_1021
20	12.2	60.0	42	9	AG218927 Drosophi
21	12.2	60.0	44	9	AG221236 Lotus cor
22	12.2	60.0	49	1	AV841468 AV841468
23	12.2	60.0	50	8	BZ583663 3590_1.54
24	11.8	59.0	25	1	AI119986 uc25501.r

AZ781782	2M0021F23	33	8	AZ781782	59.0	11.8	25	C
BM658533	TOH602767	47	4	BM658533	59.0	11.8	26	C
BJ064813	BJ064813	50	4	BJ064813	59.0	11.8	27	C
AL483587	T. brucei	27	9	AL483587	58.0	11.6	28	C
AJ594664	Arabidops	35	9	AJ594664	58.0	11.6	29	C
AJ594700	Arabidops	41	9	AJ594700	58.0	11.6	30	C
AX746801	oa52911.8	31	1	AX746801	58.0	11.6	31	C
EX893313	Arabidops	44	9	EX893313	58.0	11.6	32	C
BH791260	SALK_0592	50	8	BH791260	58.0	11.6	33	C
BJ060741	BJ060741	34	1	BJ060741	57.0	11.4	34	C
AA878482	oel5a01.8	40	1	AA878482	57.0	11.4	35	C
BH846783	SALK_0103	46	8	BH846783	57.0	11.4	36	C
AA959224	ua10H06.r	22	1	AA959224	56.0	11.2	37	C
AZ406142	IM0175G15	27	8	AZ406142	56.0	11.2	38	C
H25855	yl53h05.81	30	7	H25855	56.0	11.2	39	C
AZ611261	IM0454P22	38	8	AZ611261	56.0	11.2	40	C
AZ981274	2M0258G09	42	8	AZ981274	56.0	11.2	41	C
BZ762011	SALK_0842	42	8	BZ762011	56.0	11.2	42	C
AG198394	Pan trogl	44	9	AG198394	56.0	11.2	43	C
AL430992	T. brucei	47	9	AL430992	56.0	11.2	44	C
BH855236	SALK_0864	49	8	BH855236	56.0	11.2	45	C
AZ437556	IM0203C24	22	8	AZ437556	55.0	11.2	46	C
AZ510117	IM0354I20	24	8	AZ510117	55.0	11.2	47	C
AZ427760	IM0203P22	25	8	AZ427760	55.0	11.2	48	C
AG193210	Pan trogl	28	9	AG193210	55.0	11.2	49	C
AZ419920	IM0196E12	29	8	AZ419920	55.0	11.2	50	C
AL473241	T. brucei	30	9	AL473241	55.0	11.2	51	C
AL753260	Arabidops	31	9	AL753260	55.0	11.2	52	C
AI266818	u107d12.x	34	1	AI266818	55.0	11.2	53	C
AJ794297	AJ794297	34	1	AJ794297	55.0	11.2	54	C
AI802260	tj36907.x	37	1	AI802260	55.0	11.2	55	C
AU256811	AU256811	41	1	AU256811	55.0	11.2	56	C
AZ772195	IM0574G23	41	8	AZ772195	55.0	11.2	57	C
BH000508	2M0288L23	41	8	BH000508	55.0	11.2	58	C
AZ432986	IM0310C05	42	8	AZ432986	55.0	11.2	59	C
AZ779036	2M0014D23	42	8	AZ779036	55.0	11.2	60	C
AL761439	Arabidops	42	9	AL761439	55.0	11.2	61	C
BX650299	Arabidops	42	9	BX650299	55.0	11.2	62	C
BX656207	Arabidops	42	9	BX656207	55.0	11.2	63	C
AU256613	AU256613	43	9	AU256613	55.0	11.2	64	C
AZ818212	2M0088A11	44	8	AZ818212	55.0	11.2	65	C
AQ025360	EP(X)0804	45	9	AQ025360	55.0	11.2	66	C
AL753261	Arabidops	45	9	AL753261	55.0	11.2	67	C
AI723297	fc35d02.x	46	1	AI723297	55.0	11.2	68	C
AV838494	AV838494	46	1	AV838494	55.0	11.2	69	C
T63385	YC07C02.r1	47	7	T63385	55.0	11.2	70	C
CA964267	CCLL03a11	48	6	CA964267	55.0	11.2	71	C
AZ486468	IM0314E04	48	6	AZ486468	55.0	11.2	72	C
AA472453	vh05908.r	49	1	AA472453	55.0	11.2	73	C
AA472860	vd59c05.r	49	1	AA472860	55.0	11.2	74	C
AJ596477	Arabidops	49	9	AJ596477	55.0	11.2	75	C
AU103231	AU103231	50	1	AU103231	55.0	11.2	76	C
AU103676	AU103676	50	1	AU103676	55.0	11.2	77	C
AU103764	AU103764	50	1	AU103764	55.0	11.2	78	C
CD681923	tj33e09.y	50	6	CD681923	55.0	11.2	79	C
BH409874	1007014H1	50	8	BH409874	55.0	11.2	80	C
AL769863	Arabidops	50	9	AL769863	55.0	11.2	81	C
AL950297	Arabidops	50	9	AL950297	55.0	11.2	82	C
CG801160	1118018C0	50	9	CG801160	55.0	11.2	83	C
AZ981226	2M0258001	50	8	AZ981226	55.0	11.2	84	C
BM397244	5009-0-3-	54.0	4	BM397244	54.0	10.8	85	C
AZ873775	2M0187110	54.0	32	AZ873775	54.0	10.8	86	C
CL527787	EY05132-5	54.0	33	CL527787	54.0	10.8	87	C
BZ663500	SALK_0270	54.0	38	BZ663500	54.0	10.8	88	C
H55136	CHR220075 C	54.0	39	H55136	54.0	10.8	89	C
AA237443	mw95601.r	54.0	40	AA237443	54.0	10.8	90	C
BW504656	BW504656	54.0	40	BW504656	54.0	10.8	91	C
AZ959869	2M0227N12	54.0	41	AZ959869	54.0	10.8	92	C
AJ798572	AJ798572	54.0	41	AJ798572	54.0	10.8	93	C
AZ939796	2M0198M21	54.0	42	AZ939796	54.0	10.8	94	C
AZ627021	IM0467P13	54.0	44	AZ627021	54.0	10.8	95	C
AG197655	Pan trogl	54.0	44	AG197655	54.0	10.8	96	C

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 16:54:30 ; Search time 173.048 seconds  
(without alignments)  
684.175 Million cell updates/sec

Title: US-10-712-882A-4

Perfect score: 20

Sequence: 1 gtttagaatcttcccactt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : N Geneseqn\_16Dec04.\*

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- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
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- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	Aat13886
2	20	100.0	20	2	Aav60233
3	20	100.0	20	2	Aav32392
4	20	100.0	20	2	Aaz10703
5	20	100.0	20	2	Aax75916
6	20	100.0	20	2	Aax16616
7	20	100.0	20	2	Abx15544
8	20	100.0	20	3	Aaz37205
9	20	100.0	20	3	AAAG1920
10	20	100.0	20	4	AAF62533
11	20	100.0	20	4	AAF27681
12	20	100.0	20	5	AAC89176
13	20	100.0	20	5	AAc91422
14	20	100.0	20	6	ABN86445
15	20	100.0	20	6	AAD35206
16	20	100.0	20	6	AAD27386
17	20	100.0	20	8	AA154498
18	20	100.0	20	10	AAAS1452
19	20	100.0	20	12	ADL83326
20	20	100.0	20	12	ADN48855

21	20	100.0	20	12	AD035275
22	14.8	74.0	20	10	AB084448
23	14.2	71.0	25	2	AAT71962
24	14.2	71.0	25	2	AAT72034
25	14.2	71.0	25	9	ACI67953
26	14.2	71.0	27	2	AAQ65945
27	14	70.0	48	6	ABZ00871
28	13.8	69.0	27	6	ABN85150
29	13.8	69.0	42	10	ADC24680
30	13.8	69.0	42	10	ADC24679
31	13.8	69.0	45	10	AAU56173
32	13.8	69.0	48	2	AAAX26805
33	13.6	68.0	25	9	ACH56536
34	13.4	67.0	31	12	ADF31108
35	13.2	66.0	20	8	ABV76814
36	13.2	66.0	20	8	ABV76817
37	13.2	66.0	25	9	ACI89153
38	13.2	66.0	25	9	ACH53744
39	13.2	66.0	26	6	ABK11409
40	13.2	66.0	33	8	ACC71869
41	13.2	66.0	47	8	ACC71873
42	13	65.0	20	2	AAAX2400
43	13	65.0	41	4	AAH76405
44	12.8	64.0	19	10	ADG36386
45	12.8	64.0	19	10	ADG36387
46	12.8	64.0	20	2	AAAX83587
47	12.8	64.0	20	6	ADJ38326
48	12.8	64.0	20	6	ADJ36365
49	12.8	64.0	20	10	ADD31142
50	12.8	64.0	21	2	AAZ26058
51	12.8	64.0	21	13	ADR05251
52	12.8	64.0	22	2	AAV30750
53	12.8	64.0	25	9	ACI38734
54	12.8	64.0	25	9	ACI38106
55	12.8	64.0	41	6	ABZ44767
56	12.8	64.0	41	6	ABZ47264
57	12.6	63.0	15	6	ABN81422
58	12.6	63.0	20	2	AAZ37687
59	12.6	63.0	20	4	AAF80841
60	12.6	63.0	20	5	AAZ29456
61	12.6	63.0	20	10	ADD21652
62	12.6	63.0	23	4	AAAF29788
63	12.6	63.0	24	2	AAQ35495
64	12.6	63.0	24	5	AAZ21996
65	12.6	63.0	25	9	ACI19166
66	12.6	63.0	25	9	ACI67952
67	12.6	63.0	25	9	ACI52810
68	12.6	63.0	25	9	ACI92360
69	12.6	63.0	25	9	ACI63814
70	12.6	63.0	25	12	AD011277
71	12.6	63.0	29	2	AAT09317
72	12.6	63.0	29	3	AAV72596
73	12.6	63.0	29	12	ADI82667
74	12.6	63.0	29	13	ADSO0137
75	12.6	63.0	30	6	ABV73522
76	12.6	63.0	30	13	ADP81646
77	12.6	63.0	32	10	ADD15854
78	12.6	63.0	32	10	ADD15851
79	12.6	63.0	41	6	ABZ25044
80	12.6	63.0	41	6	ABZ43412
81	12.6	63.0	41	6	ABZ49684
82	12.6	63.0	41	6	ABZ48966
83	12.6	63.0	41	6	ABZ43533
84	12.6	63.0	44	2	AAV80370
85	12.6	63.0	50	6	ABZ07252
86	12.4	62.0	15	4	AAAF48249
87	12.4	62.0	15	4	AAAF48248
88	12.4	62.0	17	8	ACD55509
89	12.4	62.0	17	8	ACD54594
90	12.4	62.0	17	12	ADM60154
91	12.4	62.0	17	12	ADM59803
92	12.4	62.0	20	12	ADJ45328
93	12.4	62.0	20	12	ADJ45272

Ado35275 Human int  
Abq84448 DPP10 PCR  
Aat71962 Primer de  
Aat72034 Primer de  
Aci67953 Human mic  
Aaq65945 COL2A1 5'  
Abz00871 Human leu  
Abn85150 HIV gp41  
Adc24680 HIV gp41  
Adc24679 HIV gp41  
Aal56173 HIV gp 16  
Aax26805 Primer fo  
Ach56536 DNA targe  
Adf31108 E. coli b  
Abv76814 PCR prime  
Abv76817 PCR prime  
Aci89153 Human mic  
Ach53744 DNA targe  
Abk11409 E. coli p  
Acc71869 S. cerevi  
Acc71873 S. cerevi  
Aax2400 PCR prime  
Aan76405 GTP enzy  
Adg36386 HIV siNA  
Adg36387 HIV siNA  
Aax83587 Primer #1  
Aad38326 Human DLS  
Aad36365 Human DLS  
Add31142 Human mic  
Aaz26058 Human pol  
Adr05251 Human hem  
Aav30750 Telomeras  
Aci38734 Human mic  
Aci38106 Human mic  
Abz44767 Human ATP  
Abn81422 Human HTA  
Aaz37687 Human mdm  
Aaf80841 Human mdm  
Aaz29456 Human mdm  
Add21652 Human mdm  
Aaf29788 Preenili  
Aaq35495 HIV-1 det  
Aae21996 Human COL  
Aci19166 Human mic  
Aci67952 Human mic  
Aci52810 Human mic  
Aci92360 Human mic  
Aci63814 Human mic  
Ado11277 Single mu  
Aat09317 p53 gene  
Aav72596 PCR prime  
Adi82667 Human p53  
Adso0137 Human p53  
Abv73522 Human cyt  
Adp81646 Human Cyt  
Add15854 K-ras tar  
Add15851 K-ras tar  
Abz25044 Histidyl-  
Abz43412 Human ald  
Abz49684 Human SUL  
Abz48966 Human ald  
Abz43533 Human SUL  
Aav80370 Heteropol  
Abz07252 Human leu  
Aaf48249 IGFBP3 ol  
Aaf48248 IGFBP3 ol  
Acd55509 HBV ambaz  
Acd54594 HBV DNazyl  
Adm60154 Hepatitis  
Adm59803 Hepatitis  
Adj45328 Hepatoma-  
Adj45272 Hepatoma-

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OM nucleic - nucleic search, using sw model  
Run on: October 6, 2005, 18:41:56 ; Search time 694.476 Seconds  
(without alignments)  
1395.446 Million cell updates/sec

Title: US-10-712-882A-4  
Perfect score: 20  
Sequence: 1 gtttagaatcttccactt 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.hcg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	6	A82472 Sequence 10
2	20	100.0	20	6	AR116899 Sequence
3	20	100.0	20	6	AR144077 Sequence
4	20	100.0	20	6	AR159626 Sequence
5	20	100.0	20	6	BD185756 Method an
6	20	100.0	20	6	BD246776 Diagnosti
7	20	100.0	20	6	BD246786 Diagnosti
8	20	100.0	20	6	I73228 Sequence 4
9	20	100.0	20	6	AR282882 Sequence
10	20	100.0	20	6	AR307522 Sequence
11	20	100.0	20	6	AR487080 Sequence
12	20	100.0	20	6	AR490512 Sequence
13	20	100.0	20	6	AR493811 Sequence
14	20	100.0	20	6	AR532955 Sequence
15	20	100.0	20	6	AR534177 Sequence
16	20	100.0	20	6	AR542776 Sequence
17	20	100.0	20	6	AX012490 Sequence
18	20	100.0	20	6	AX052794 Sequence
19	20	100.0	20	6	AX067281 Sequence

20	20	100.0	20	6	AX080609 Sequence
21	20	100.0	20	6	AX360024 Sequence
22	20	100.0	20	6	AX463194 Sequence
23	20	100.0	20	6	AX469449 Sequence
24	20	100.0	20	6	BD070855 Predictio
25	20	100.0	20	6	BD085840 Methods o
26	20	100.0	20	6	BD124533 Predictio
27	14.8	74.0	20	6	AX590794 Sequence
28	14.2	71.0	27	6	AR072383 Sequence
29	14.2	71.0	27	6	I26494 Sequence 18
30	13.8	69.0	42	6	AX766392 Sequence
31	13.8	69.0	42	6	AX766393 Sequence
32	13.8	69.0	48	6	AR491580 Sequence
33	13.6	68.0	38	6	I05583 Sequence 14
34	13.2	66.0	20	6	BD179437 Genomic D
35	13.2	66.0	20	6	BD179440 Genomic D
36	13.2	66.0	20	6	AX752731 Sequence
37	13.2	66.0	42	12	ASE011054 Artificial
38	13.2	66.0	47	6	AR288599 Sequence
39	13.2	66.0	47	6	AX752735 Sequence
40	13	65.0	20	6	AR311164 Sequence
41	13	65.0	40	6	AI3297 oligonucleo
42	12.8	64.0	20	6	E31395 Method for
43	12.8	64.0	20	6	E31395 Method for
44	12.8	64.0	20	6	AX412185 Sequence
45	12.8	64.0	22	6	E36979 Human telom
46	12.8	64.0	22	6	AR243500 Sequence
47	12.8	64.0	22	6	AR390656 Sequence
48	12.8	64.0	22	6	AR393270 Sequence
49	12.8	64.0	22	6	AX810561 Sequence
50	12.8	64.0	22	6	BD011230 Human tel
51	12.8	64.0	41	6	AX515353 Sequence
52	12.8	64.0	41	6	AX517850 Sequence
53	12.6	63.0	20	6	BD138291 Antisense
54	12.6	63.0	24	6	I12747 Sequence 45
55	12.6	63.0	29	6	CQ779652 Sequence
56	12.6	63.0	29	6	AR452553 Sequence
57	12.6	63.0	41	6	AX521221 Sequence
58	12.2	61.0	20	6	AR213923 Sequence
59	12.2	61.0	20	6	AX487535 Sequence
60	12.2	61.0	21	6	AX117191 Sequence
61	12.2	61.0	21	6	AX417518 Sequence
62	12.2	61.0	24	6	AX297574 Sequence
63	12.2	61.0	26	6	AR164899 Sequence
64	12.2	61.0	26	6	AR490700 Sequence
65	12.2	61.0	26	6	AR532473 Sequence
66	12.2	61.0	30	6	AX003496 Sequence
67	12.2	61.0	30	6	BD087112 Erythrovi
68	12.2	61.0	36	3	CEANONYFR X97532 C.elegans D
69	12.2	61.0	37	6	A91222 Sequence 14
70	12.2	61.0	37	6	AR000548 Sequence
71	12.2	61.0	37	6	AR076143 Sequence
72	12.2	61.0	37	6	AR145089 Sequence
73	12.2	61.0	37	6	BD056480 Proteins
74	12.2	61.0	39	6	AR182875 Sequence
75	12.2	61.0	39	6	AR533652 Sequence
76	12.2	61.0	39	6	AR533653 Sequence
77	12.2	61.0	39	6	AX799172 Sequence
78	12.2	61.0	39	6	AX799173 Sequence
79	12.2	61.0	40	6	AR076442 Sequence
80	12.2	61.0	40	6	AR106042 Sequence
81	12.2	61.0	41	6	AX513998 Sequence
82	12.2	61.0	41	6	AX514119 Sequence
83	12.2	61.0	41	6	AX514134 Sequence
84	12.2	61.0	41	6	AX519551 Sequence
85	12.2	61.0	41	6	AX520268 Sequence
86	12.2	61.0	41	6	AX520285 Sequence
87	12.2	61.0	42	6	BD266496 Universal
88	12.2	61.0	47	6	AR291201 Sequence
89	12.2	61.0	49	6	AR079732 Sequence
90	12.2	61.0	49	6	AR081262 Sequence
91	12.2	61.0	49	6	AR170622 Sequence
92	12	60.0	17	6	AX760866 Sequence

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	20	100.0	20	9	US-09-852-948-1	Sequence 16, Appli
2	20	100.0	20	9	US-09-845-129-15	Sequence 16, Appl
3	20	100.0	20	10	US-09-950-935-14	Sequence 14, Appl
4	20	100.0	20	10	US-09-888-056A-9	Sequence 9, Appli
5	20	100.0	20	13	US-10-032-242A-1	Sequence 1, Appli
6	20	100.0	20	15	US-10-167-127-19	Sequence 19, Appli
7	20	100.0	20	16	US-10-172-919-28	Sequence 28, Appli

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:11:51 ; Search time 49.0476 Seconds  
(without alignments)  
667.220 Million cell updates/sec

Title: US-10-712-882A-3

Perfect score: 20

Sequence: 1 tggcattgattcgttcac 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents NA.\*

1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	US-08-510-696-3
2	20	100.0	20	3	US-09-005-923-3
3	20	100.0	20	3	US-08-813-456-3
4	20	100.0	20	3	US-09-183-850-1
5	20	100.0	20	3	US-09-345-217-16
6	20	100.0	20	4	US-09-431-352-5
7	20	100.0	20	4	US-09-852-948-1
8	20	100.0	20	4	US-09-845-129-16
9	20	100.0	20	4	US-09-037-472-3
10	20	100.0	20	4	US-09-578-534-3
11	20	100.0	20	4	US-09-632-657-17
12	20	100.0	20	4	US-09-693-555A-3
13	20	100.0	20	4	US-09-584-950-11
14	20	100.0	20	5	PCT-US96-12455-3
15	14.2	71.0	20	3	US-08-397-220B-56
16	14.2	71.0	20	3	US-08-650-093C-56
17	14.2	71.0	23	1	US-08-356-287-1
18	14.2	71.0	23	5	PCT-US93-04863-1
19	14.2	71.0	48	4	US-09-782-361-49
20	13.6	68.0	20	4	US-09-396-196G-62659
21	13.6	68.0	25	4	US-09-396-196G-62669
22	13.6	68.0	45	1	US-08-176-412-4
23	13.6	68.0	45	2	US-08-555-268A-4
24	13.6	68.0	45	2	US-08-495-695B-4
25	13.6	68.0	45	5	PCT-US94-14436-4
26	13.6	68.0	48	1	US-08-429-181-28
27	13.6	68.0	48	1	US-08-164-388-28

Sequence 18, Appl	20	3	US-09-318-191-18	67.0	13.4	C	28
Sequence 29, Appl	25	3	US-09-335-409-29	66.0	13.2	C	29
Sequence 29, Appl	25	3	US-09-568-102-29	66.0	13.2	C	30
Sequence 29, Appl	25	3	US-09-567-969-29	66.0	13.2	C	31
Sequence 29, Appl	25	3	US-09-568-480-29	66.0	13.2	C	32
Sequence 29, Appl	25	3	US-09-568-486-29	66.0	13.2	C	33
Sequence 29, Appl	25	3	US-09-568-472-29	66.0	13.2	C	34
Sequence 29, Appl	25	3	US-09-567-899-29	66.0	13.2	C	35
Sequence 53, Appl	31	1	US-08-591-070A-53	66.0	13.2	C	36
Sequence 53, Appl	31	1	US-08-927-855-53	66.0	13.2	C	37
Sequence 48, Appl	33	1	US-08-438-639-48	66.0	13.2	C	38
Sequence 48, Appl	33	1	US-07-813-338A-48	66.0	13.2	C	39
Sequence 58, Appl	33	2	US-08-470-124-58	66.0	13.2	C	40
Sequence 124, App	33	3	US-08-441-971-124	66.0	13.2	C	41
Sequence 124, App	33	3	US-08-221-653-124	66.0	13.2	C	42
Sequence 124, App	33	3	US-08-442-144A-124	66.0	13.2	C	43
Sequence 124, App	33	3	US-08-441-970-124	66.0	13.2	C	44
Sequence 15, Appl	27	4	US-09-638-544-15	65.0	13	C	45
Sequence 21, Appl	27	5	PCT-US94-10957-21	65.0	13	C	46
Sequence 57, Appl	20	3	US-09-780-049-57	64.0	12.8	C	47
Sequence 27819, A	25	4	US-09-396-196G-27819	64.0	12.8	C	48
Sequence 33646, A	25	4	US-09-396-196G-33646	64.0	12.8	C	49
Sequence 51966, A	25	4	US-09-396-196G-51966	64.0	12.8	C	50
Sequence 55924, A	25	4	US-09-396-196G-55924	64.0	12.8	C	51
Sequence 58, Appl	29	4	US-09-396-154-58	64.0	12.8	C	52
Sequence 739, App	22	4	US-09-422-978-739	63.0	12.6	C	53
Sequence 101, App	22	4	US-09-090-672B-101	63.0	12.6	C	54
Sequence 13, Appl	24	4	US-10-071-411A-13	63.0	12.6	C	55
Sequence 20711, A	25	4	US-09-396-196G-20711	63.0	12.6	C	56
Sequence 37508, A	25	4	US-09-396-196G-37508	63.0	12.6	C	57
Sequence 78105, A	25	4	US-09-396-196G-78105	63.0	12.6	C	58
Sequence 90591, A	25	4	US-09-396-196G-90591	63.0	12.6	C	59
Sequence 90593, A	25	4	US-09-396-196G-90593	63.0	12.6	C	60
Sequence 102789, A	25	4	US-09-396-196G-102789	63.0	12.6	C	61
Sequence 122911, A	25	4	US-09-396-196G-122911	63.0	12.6	C	62
Sequence 55, Appl	30	3	US-09-608-285A-55	63.0	12.6	C	63
Sequence 30, Appl	33	3	US-08-974-022-30	63.0	12.6	C	64
Sequence 30, Appl	33	3	US-08-795-445A-30	63.0	12.6	C	65
Sequence 30, Appl	33	3	US-08-795-447A-30	63.0	12.6	C	66
Sequence 30, Appl	33	3	US-08-974-186-30	63.0	12.6	C	67
Sequence 30, Appl	33	3	US-08-795-446B-30	63.0	12.6	C	68
Sequence 23, Appl	33	3	US-08-706-945D-23	63.0	12.6	C	69
Sequence 30, Appl	33	4	US-08-577-788C-30	63.0	12.6	C	70
Sequence 962, App	47	4	US-09-422-978-962	63.0	12.6	C	71
Sequence 2694, Ap	50	4	US-09-270-767-2694	63.0	12.6	C	72
Sequence 25514, A	19	3	US-09-195-817-5	62.0	12.4	C	73
Sequence 5, Appl	20	1	US-08-715-142-5	62.0	12.4	C	74
Sequence 25, Appl	20	1	US-08-715-142-25	62.0	12.4	C	75
Sequence 4294, Ap	20	4	US-09-198-452A-4294	62.0	12.4	C	76
Sequence 16170, A	25	4	US-09-396-196G-16170	62.0	12.4	C	77
Sequence 104493, A	25	4	US-09-396-196G-104493	62.0	12.4	C	78
Sequence 10493, A	25	4	US-09-396-196G-10493	62.0	12.4	C	79
Sequence 6, Appl	25	4	US-09-601-645A-6	62.0	12.4	C	80
Sequence 44, Appl	34	2	US-08-318-157B-44	62.0	12.4	C	81
Sequence 8, Appl	34	4	US-08-435-516-8	62.0	12.4	C	82
Sequence 44, Appl	34	4	US-08-446-668-44	62.0	12.4	C	83
Sequence 6, Appl	35	3	US-09-253-794-6	62.0	12.4	C	84
Sequence 10, Appl	35	4	US-09-581-472B-10	62.0	12.4	C	85
Sequence 3, Appl	36	2	US-08-678-194-3	62.0	12.4	C	86
Sequence 3, Appl	36	3	US-08-890-011-3	62.0	12.4	C	87
Sequence 3, Appl	36	3	US-09-262-724-3	62.0	12.4	C	88
Patent No. 5187077	36	6	5187077-2	62.0	12.4	C	89
Patent No. 5427925	36	6	5427925-2	62.0	12.4	C	90
Patent No. 5187077	36	6	5187077-2	62.0	12.4	C	91
Patent No. 5427925	36	6	5427925-2	62.0	12.4	C	92
Sequence 7, Appl	37	3	US-08-446-668-7	62.0	12.4	C	93
Sequence 3, Appl	20	1	US-08-356-287-3	61.0	12.2	C	94
Sequence 22, Appl	20	3	US-09-435-296-22	61.0	12.2	C	95
Sequence 3, Appl	20	5	PCT-US93-04863-3	61.0	12.2	C	96
Sequence 4, Appl	21	3	US-08-397-220B-4	61.0	12.2	C	97
Sequence 4, Appl	21	3	US-08-650-093C-4	61.0	12.2	C	98
Sequence 4, Appl	21	3	US-08-823-895A-4	61.0	12.2	C	99
Sequence 4, Appl	21	3	US-08-823-895A-4	61.0	12.2	C	100

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:46:26 ; Search time 1296.76 Seconds  
(without alignments)  
587.066 Million cell updates/sec

Title: US-10-712-882A-3

Perfect score: 20  
Sequence: 1 tggcattgattggttcac 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database: EST.\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_hic.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_gsi1.\*
- 9: gb\_gsi2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	13.4	67.0	42	9	CL518282
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3	12.6	63.0	50	8	AZ498776
4	12.4	62.0	50	9	AG242574
5	12.2	61.0	49	8	BZ594191
6	12.2	60.0	35	7	T60615
7	12.2	60.0	41	8	BH866191
8	12.2	60.0	46	1	AI790825
9	12.2	60.0	47	8	AZ793177
10	12.2	60.0	48	8	BH790271
11	11.8	59.0	21	9	AG203325
12	11.8	59.0	25	8	AZ871751
13	11.8	59.0	34	8	AZ658779
14	11.6	59.0	50	9	CR044265
15	11.6	58.0	29	9	CL682929
16	11.6	58.0	30	8	CC457826
17	11.6	58.0	43	8	AZ370403
18	11.6	58.0	44	7	D67719
19	11.6	58.0	45	9	TA185A11P
20	11.6	58.0	46	9	AG213917
21	11.6	58.0	48	1	AJ666395
22	11.6	58.0	49	1	AI047702
23	11.4	57.0	22	8	AZ982706
24	11.4	57.0	43	8	BH907510

C	25	11.4	57.0	46	7	R89440
C	26	11.4	57.0	47	8	AZ435382
C	27	11.2	56.0	29	9	CC797798
C	28	11.2	56.0	34	9	CC868895
C	29	11.2	56.0	36	9	CL210852
C	30	11.2	56.0	38	6	CD745048
C	31	11.2	56.0	38	9	AJ590231
C	32	11.2	56.0	40	8	AZ433386
C	33	11.2	56.0	40	9	AJ599139
C	34	11.2	56.0	41	9	CC794463
C	35	11.2	56.0	43	8	BH857448
C	36	11.2	56.0	45	9	CNS07H2F
C	37	11.2	56.0	46	8	AZ791856
C	38	11.2	56.0	48	1	AV834340
C	39	11.2	56.0	49	1	AI035265
C	40	11.2	56.0	49	8	AZ800706
C	41	11.2	55.0	20	1	AJ789573
C	42	11.2	55.0	31	7	H22517
C	43	11.2	55.0	31	9	AG202529
C	44	11.2	55.0	35	5	BW591074
C	45	11.2	55.0	37	9	CL436859
C	46	11.2	55.0	38	8	AZ774356
C	47	11.2	55.0	38	8	BH792827
C	48	11.2	55.0	41	8	AZ579388
C	49	11.2	55.0	43	7	T61017
C	50	11.2	55.0	45	8	BH865166
C	51	11.2	55.0	45	8	CC037129
C	52	11.2	55.0	45	9	EX652140
C	53	11.2	55.0	47	6	CA584498
C	54	11.2	55.0	47	8	BZ766487
C	55	11.2	55.0	48	7	Z20559
C	56	11.2	55.0	48	9	AJ591318
C	57	11.2	55.0	49	1	AI444429
C	58	11.2	55.0	49	8	BH803126
C	59	11.2	55.0	50	1	AU102915
C	60	11.2	55.0	50	1	AU102917
C	61	11.2	55.0	50	1	AU102918
C	62	11.2	55.0	50	7	CN478129
C	63	10.8	54.0	23	8	AZ658079
C	64	10.8	54.0	26	8	BH901105
C	65	10.8	54.0	30	8	AZ969026
C	66	10.8	54.0	30	9	AG194048
C	67	10.8	54.0	32	2	AW688792
C	68	10.8	54.0	35	8	AZ486905
C	69	10.8	54.0	35	9	CC796535
C	70	10.8	54.0	36	8	AZ659063
C	71	10.8	54.0	36	8	BZ379504
C	72	10.8	54.0	37	8	BZ379503
C	73	10.8	54.0	41	2	AV966744
C	74	10.8	54.0	42	9	AG203682
C	75	10.8	54.0	43	9	CG869098
C	76	10.8	54.0	44	9	AZ345620
C	77	10.8	54.0	44	9	TA184G10Q
C	78	10.8	54.0	49	1	AA026164
C	79	10.8	54.0	49	1	AI529812
C	80	10.8	54.0	49	8	BH812148
C	81	10.8	54.0	49	8	CC038341
C	82	10.8	54.0	50	8	AZ666536
C	83	10.8	54.0	50	8	CC794052
C	84	10.6	53.0	27	9	AZ832643
C	85	10.6	53.0	33	9	BX655891
C	86	10.6	53.0	37	1	AA865423
C	87	10.6	53.0	37	9	CL655997
C	88	10.6	53.0	38	9	CL531222
C	89	10.6	53.0	38	9	AZ831353
C	90	10.6	53.0	39	1	TA10A12Q
C	91	10.6	53.0	40	1	AV851328
C	92	10.6	53.0	40	8	AZ307537
C	93	10.6	53.0	40	8	BH856041
C	94	10.6	53.0	41	8	BZ377662
C	95	10.6	53.0	42	8	AZ785539
C	96	10.6	53.0	43	7	W11348
C	97	10.6	53.0	43	7	W11348

R89440 yq05a01.r1  
AZ435382 IM0222D23  
CC797798 SALK\_1454  
CC868895 SALK\_1492  
CL210852 W040B04 G  
CD745048 RB8 A09 R  
AJ590231 Arabidops  
AZ433386 IM0219A14  
AJ599139 Arabidops  
CC794463 SALK\_0492  
BH857448 SALK\_0748  
AL610521 Anopheles  
AZ791856 2M0041L19  
AV834340 AV834340  
AI035265 ue18p08.x  
AZ800706 2M0058D24  
AJ789573 AJ789573  
H22517 yn69b10.r1  
AG202529 Pan trogl  
BW591074 BW591074  
CL436859 PST1986-N  
AZ774356 2M0003B07  
BH792827 SALK\_0650  
AZ579388 IM0363P15  
T61017 yb74b06.r1  
BH865166 SALK\_0974  
CC037129 3591\_1.85  
EX652140 Arabidops  
CA584498 LBB00786.  
BZ766487 SALK\_1374  
Z20559 HSAACKCU T  
AJ591318 Arabidops  
AI444429 fb38d01.x  
BH803126 1008100E1  
AU102915 AU102915  
AU102917 AU102917  
AU102918 AU102918  
CN478129 rx46e01.y  
AZ658079 IM0534H11  
BH901105 KG98833-5  
AZ969026 2M0241E12  
AG194048 Pan trogl  
AW688792 r378 non-  
AZ486905 IM0316N09  
CC796535 SALK\_1323  
AZ659063 IM0536N10  
BZ379504 SALK\_1134  
BZ379503 SALK\_1134  
AV966744 AV966744  
AG203682 Pan trogl  
W87658 zh67e12.s1  
CG869098 AC0059.Sa  
AZ345620 IM0080R24  
AL473645 T. brucei  
AA026164 ze94f03.s  
AI529812 ui82g04.y  
BH812148 SALK\_0612  
CC038341 3591\_1.94  
AZ666536 IM0548D16  
CC794052 SALK\_0406  
AZ832643 2M0113A22  
BX655891 Arabidops  
AX865423 oh29d10.s  
AM531222 nj52c12.s  
CL655997 PRI0125b  
AZ831353 2M011K01  
AL461772 T. brucei  
AV851328 AV851328  
AZ307537 IM0003P20  
BH856041 SALK\_0834  
BZ377662 SALK\_0987  
AZ785539 2M0029C03  
W11348 ma78g04.r1

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 16:54:30 ; Search time 173.048 Seconds  
(without alignments)  
684.175 Million cell updates/sec

Title: US-10-712-882A-3

Perfect score: 20

Sequence: 1 tggcattgatctggttcac 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : N Geneseq 16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	Aat13885 Primer fo
2	20	100.0	20	2	AAV60232 PCR prime
3	20	100.0	20	2	Aav32391 Interleuk
4	20	100.0	20	2	Aax75915 Human int
5	20	100.0	20	2	Aax16615 Interleuk
6	20	100.0	20	2	Abx15543 Human IL-
7	20	100.0	20	3	Aaz37204 PCR prime
8	20	100.0	20	3	Aaa61919 Human IL-
9	20	100.0	20	4	Aaf27680 Primer #1
10	20	100.0	20	5	Aac89175 Human IL-
11	20	100.0	20	5	Aac91421 Human IL-
12	20	100.0	20	6	Abn86444 IL-1beta
13	20	100.0	20	6	Aad35205 Human IL1
14	20	100.0	20	6	Aad27385 PCR prime
15	20	100.0	20	8	Aal54497 Ageing-re
16	20	100.0	20	10	AAD51451
17	20	100.0	20	12	ADL83325
18	20	100.0	20	12	ADNA48854
19	20	100.0	20	12	ADO35274 Human int
20	18	90.0	18	4	Aaf62532 Primer #5

c	21	15.2	76.0	50	6	ABZ07795
c	22	14.8	74.0	20	12	ADQ15376
c	23	14.4	72.0	41	6	ABZ25031
c	24	14.2	71.0	19	10	ADF51817
c	25	14.2	71.0	19	10	ADF52513
c	26	14.2	71.0	19	10	ADFI41427
c	27	14.2	71.0	19	12	ADO43692
c	28	14.2	71.0	20	2	AAQ58418
c	29	14.2	71.0	20	2	AAT80304
c	30	14.2	71.0	20	6	ABS65888
c	31	14.2	71.0	20	12	ADO43698
c	32	14.2	71.0	23	2	AAQ53233
c	33	14.2	71.0	23	12	ADP87813
c	34	14.2	71.0	25	13	ADS34695
c	35	14.2	71.0	26	12	ADP87789
c	36	14.2	71.0	26	12	ADP87790
c	37	14.2	71.0	26	12	ADP87797
c	38	14.2	71.0	30	2	AAQ21855
c	39	14.2	71.0	38	10	ADC54057
c	40	14.2	71.0	40	10	ADC46967
c	41	14.2	71.0	40	12	ADP87794
c	42	14.2	71.0	43	3	AAA87096
c	43	14.2	71.0	48	10	ACD27597
c	44	14	70.0	20	4	AAH22924
c	45	13.8	69.0	25	12	ADP14042
c	46	13.8	69.0	25	12	ADP14041
c	47	13.6	68.0	42	6	ABA98853
c	48	13.6	68.0	45	2	AAQ94174
c	49	13.6	68.0	48	2	AAQ98118
c	50	13.4	67.0	20	2	AAQ44490
c	51	13.4	67.0	20	6	ABQ93115
c	52	13.4	67.0	23	12	ADK95452
c	53	13.4	67.0	24	12	ADK95427
c	54	13.4	67.0	25	4	AAH37927
c	55	13.4	67.0	25	9	ACI23573
c	56	13.2	66.0	19	10	ADF51810
c	57	13.2	66.0	19	10	ADF52512
c	58	13.2	66.0	19	10	ADF51816
c	59	13.2	66.0	19	10	ADF52506
c	60	13.2	66.0	19	12	ADP87812
c	61	13.2	66.0	20	10	ADBI4481
c	62	13.2	66.0	22	12	ADP87785
c	63	13.2	66.0	23	12	ADP87805
c	64	13.2	66.0	25	3	AAZ55893
c	65	13.2	66.0	26	12	ADP87784
c	66	13.2	66.0	31	2	AAI32804
c	67	13.2	66.0	31	2	AAI32803
c	68	13.2	66.0	32	3	AAI32803
c	69	13.2	66.0	32	3	AAI32803
c	70	13.2	66.0	33	2	AAQ46461
c	71	13.2	66.0	33	2	AAV07835
c	72	13.2	66.0	33	2	AAV83063
c	73	13.2	66.0	50	4	AAI34211
c	74	13	65.0	24	10	ADD13772
c	75	13	65.0	27	2	AAQ86382
c	76	13	65.0	27	4	AAF84287
c	77	13	65.0	27	8	AAF76179
c	78	13	65.0	27	8	ACC42615
c	79	12.8	64.0	20	6	ABS65438
c	80	12.8	64.0	20	12	ADM80290
c	81	12.8	64.0	20	13	ADS12560
c	82	12.8	64.0	22	12	ADO07404
c	83	12.8	64.0	25	5	AAI62242
c	84	12.8	64.0	25	12	ADP14043
c	85	12.8	64.0	25	13	ADP56622
c	86	12.8	64.0	29	4	AAQ00915
c	87	12.8	64.0	33	6	ABZ25028
c	88	12.8	64.0	41	6	ABZ25030
c	89	12.8	64.0	42	2	AAV51012
c	90	12.6	63.0	20	12	ADJ61456
c	91	12.6	63.0	20	12	ADO46846
c	92	12.6	63.0	20	12	ADO46844
c	93	12.6	63.0	21	8	ABT34008

Abz07795	Human leu
Adq15376	Human thy
Abz25031	Integrin
Adf51817	Hepatitis
Adf52513	Hepatitis
Adi41427	Primer HC
Ado43692	Antisense
Aa58418	Antisense
Aat80304	Oligo HCV
Abz65888	Inhibitor
Ado43698	Antisense
Aa53233	Hepatitis
Adp87813	Extended
Adp34695	Primer Ds
Adp87789	TEX synth
Adp87790	TEX on mi
Adp87797	Extended
Aa21855	HCV probe
Adc54057	Genotype
Adc46967	Synthesis
Adp87794	HCV CDNA
Aa87096	Rat hepat
Adc27597	Hepatitis
Ah22924	Interleuk
Adp14042	Renal cel
Adp14041	Renal cel
Abz98853	PCR prime
Aa94174	Transmemb
Aa98118	Label ext
Aa44490	HCV virus
Abq93115	T. tausch
Adk95452	Primer of
Adk95427	Primer of
Aah37927	SNP speci
Ac123573	Human mic
Adf51810	Hepatitis
Adf52512	Hepatitis
Adf51816	Hepatitis
Adf52506	Hepatitis
Adp87812	Extended
Adel4481	HSP11B1 a
Adp87785	TEX exten
Adp87805	TEX termi
Aaz55893	Sorangium
Adp8784	TEX synth
Aax32804	Human mpl
Aax32803	Human mpl
Aac8579	Target st
Aac8578	Target st
Aa46461	Hepatitis
Aav07835	HCV.33.6
Aav83063	Amplifier
Aal34211	Human SNP
Add13772	Human PDE
Aa86382	LIF detec
Aaf84287	Human LIF
Aaf76179	Human leu
Acc42615	Human leu
Abz65438	Human/mou
Adm80290	Human GAP
Ads12560	PCR prime
Ado07404	Human hep
Aai62242	Soybean 3
Adp14043	Renal cel
Adp56622	Drug ther
Aa00915	Beetle lu
Abz25028	Integrin
Abz25030	Integrin
Aav51012	Maize pol
Adj61456	Oligonuc
Ado46846	Human oli
Ado46844	Human pig
Abt34008	Human pig

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:41:56 ; Search time 694.476 Seconds  
(without alignments)  
1395.446 Million cell updates/sec

Title: US-10-712-882A-3

Perfect score: 20  
Sequence: 1 tggcattgattcgttgcattc 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hg.\*
- 3: gb\_in.\*
- 4: gb\_on.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	6	A82471 Sequence 9
2	20	100.0	20	6	AR116898 Sequence
3	20	100.0	20	6	AR144076 Sequence
4	20	100.0	20	6	AR159625 Sequence
5	20	100.0	20	6	BD185755 Method an
6	20	100.0	20	6	BD246775 Diagnosti
7	20	100.0	20	6	BD246785 Diagnosti
8	20	100.0	20	6	I73227 Sequence 3
9	20	100.0	20	6	AR282881 Sequence
10	20	100.0	20	6	AR307521 Sequence
11	20	100.0	20	6	AR487079 Sequence
12	20	100.0	20	6	AR490511 Sequence
13	20	100.0	20	6	AR493810 Sequence
14	20	100.0	20	6	AR532954 Sequence
15	20	100.0	20	6	AR534176 Sequence
16	20	100.0	20	6	AR542775 Sequence
17	20	100.0	20	6	AX052793 Sequence
18	20	100.0	20	6	AX067280 Sequence
19	20	100.0	20	6	AX360023 Sequence

AX463193 Sequence  
AX469448 Sequence  
BD070854 Predictio  
BD085839 Methods o  
BD124532 Predictio  
AX012489 Sequence  
AX080608 Sequence  
AR167039 Sequence  
E06779 Primer to d  
AR210694 Sequence  
I73270 Sequence 1  
BD183036 Nucleic a  
AX195815 Sequence  
A01669 Nucleotide  
AJ786205 Sulfolobu  
AX428587 Sequence  
AR075911 Sequence  
AR083197 Sequence  
I20780 Sequence 4  
I44599 Sequence 28  
I71004 Sequence 28  
AR169763 Sequence  
E06777 Primer to d  
AX462639 Sequence  
AX115600 Sequence  
BD218240 Genes for  
AR193035 Sequence  
AR199557 Sequence  
AR199565 Sequence  
AR199573 Sequence  
AR201103 Sequence  
AR208677 Sequence  
L07936 Bacterioph  
AR008928 Sequence  
AR087623 Sequence  
BD080608 MPL ligan  
BD263855 Adeno-abb  
BD263856 Adeno-abb  
AX048341 Sequence  
AX048342 Sequence  
AR004394 Sequence  
AR064933 Sequence  
AR097186 Sequence  
AR130684 Sequence  
AR172033 Sequence  
I82869 Sequence 48  
CQ008779 Sequence  
AX766438 Sequence  
AX309105 Sequence  
AX138604 Sequence  
CQ0809675 Sequence  
AR236845 Sequence  
CQ865340 Sequence  
AX197166 Sequence  
AR373110 Sequence  
AX098339 Sequence  
AR289004 Sequence  
CQ802904 Sequence  
AX449795 Sequence  
AR181110 Sequence  
BD013356 Herbicide  
BD015588 Herbicide  
AX014443 Sequence  
AX014788 Sequence  
BD002581 Gene comp  
BD194392 Mimotopes  
AX009973 Sequence  
AR168754 Sequence  
AR205491 Sequence  
AR391942 Sequence  
AX076507 Sequence  
AX236861 Sequence  
BD183037 Nucleic a

20 100.0 20 6 AX463193  
21 100.0 20 6 AX469448  
22 100.0 20 6 BD070854  
23 100.0 20 6 BD085839  
24 100.0 20 6 BD124532  
25 95.0 19 6 AX012489  
26 90.0 18 6 AX080608  
27 71.0 20 6 AR167039  
28 71.0 20 6 E06779  
29 71.0 20 6 AR210694  
30 71.0 23 6 I73270  
31 71.0 38 6 BD183036  
32 70.0 20 6 AX195815  
33 70.0 35 6 A01669  
34 68.0 42 1 AJ786205  
35 68.0 42 6 AX428587  
36 68.0 45 6 AR075911  
37 68.0 45 6 AR083197  
38 68.0 45 6 I20780  
39 68.0 48 6 I44599  
40 68.0 48 6 I71004  
41 67.0 20 6 AR169763  
42 67.0 20 6 E06777  
43 67.0 20 6 AX462639  
44 67.0 25 6 AX115600  
45 66.0 25 6 BD218240  
46 66.0 25 6 AR193035  
47 66.0 25 6 AR199557  
48 66.0 25 6 AR199565  
49 66.0 25 6 AR199573  
50 66.0 25 6 AR201103  
51 66.0 25 6 AR208677  
52 66.0 30 7 PFDFRGMNT  
53 66.0 31 6 AR008928  
54 66.0 31 6 AR087623  
55 66.0 31 6 BD080608  
56 66.0 32 6 BD263855  
57 66.0 32 6 BD263856  
58 66.0 32 6 AX048341  
59 66.0 32 6 AX048342  
60 66.0 33 6 AR004394  
61 66.0 33 6 AR064933  
62 66.0 33 6 AR097186  
63 66.0 33 6 AR130684  
64 66.0 33 6 AR172033  
65 66.0 33 6 I82869  
66 66.0 50 6 CQ008779  
67 65.0 24 6 AX766438  
68 65.0 27 6 AX309105  
69 65.0 27 6 AX138604  
70 64.0 20 6 CQ0809675  
71 64.0 20 6 AR236845  
72 64.0 25 6 CQ865340  
73 64.0 25 6 AX197166  
74 64.0 29 6 AR373110  
75 64.0 29 6 AX098339  
76 64.0 47 6 AR289004  
77 63.0 25 6 CQ802904  
78 63.0 26 6 AX449795  
79 63.0 30 6 AR181110  
80 63.0 30 6 BD013356  
81 63.0 30 6 BD015588  
82 63.0 31 6 AX014443  
83 63.0 31 6 AX014788  
84 63.0 31 6 BD002581  
85 63.0 32 6 BD194392  
86 63.0 32 6 AX009973  
87 63.0 33 6 AR168754  
88 63.0 33 6 AR205491  
89 63.0 33 6 AR391942  
90 63.0 33 6 AX076507  
91 63.0 34 6 AX236861  
92 63.0 38 6 BD183037



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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:30:35 ; Search time 306.095 Seconds  
(without alignments)  
455.077 Million cell updates/sec

Title: US-10-712-882A-2

Perfect score: 20

Sequence: 1 gtacctccagatatacatt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 10399348

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications NA:\*

1: /cgn2\_6/ptodata/1/pubpna/PCT NEW PUB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT NEW PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06 NEW PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06 PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07 NEW PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08 NEW PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08 PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09 NEW PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10G PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US10H PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US10I PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US10 NEW PUB.seq.\*  
23: /cgn2\_6/ptodata/1/pubpna/US11A PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq.\*  
25: /cgn2\_6/ptodata/1/pubpna/US60 NEW PUB.seq.\*  
26: /cgn2\_6/ptodata/1/pubpna/US60 PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	21	US-10-712-882-2
2	14.2	71.0	25	15	Sequence 2, Appl1
3	14.2	71.0	25	15	Sequence 10874, A
4	14.2	71.0	25	21	Sequence 207354, A
5	14.2	71.0	25	21	Sequence 764402, A
6	14.2	71.0	25	22	Sequence 20607, A
7	13.6	68.0	25	21	Sequence 68200, A
					Sequence 897658, A

25	22	US-10-719-956-55702	68.0	13.6	Sequence 55702, A
25	22	US-10-719-956-309725	68.0	13.6	Sequence 309725, A
25	24	US-11-036-317-535566	68.0	13.6	Sequence 535566, A
25	21	US-10-719-900-347747	67.0	13.4	Sequence 347747, A
25	22	US-10-719-956-420158	67.0	13.4	Sequence 420158, A
25	24	US-11-036-317-434177	67.0	13.4	Sequence 434177, A
25	24	US-11-036-317-536744	67.0	13.4	Sequence 536744, A
20	21	US-10-831-901A-5628	66.0	13.2	Sequence 5628, Ap
20	21	US-10-831-901A-5629	66.0	13.2	Sequence 5629, Ap
21	20	US-10-751-736-13419	66.0	13.2	Sequence 13419, A
25	15	US-10-098-263B-94921	66.0	13.2	Sequence 94921, A
25	15	US-10-098-263B-94922	66.0	13.2	Sequence 94922, A
25	21	US-10-719-900-91830	66.0	13.2	Sequence 91830, A
25	21	US-10-719-900-248182	66.0	13.2	Sequence 248182, A
25	21	US-10-719-900-447647	66.0	13.2	Sequence 447647, A
25	21	US-10-719-900-676676	66.0	13.2	Sequence 676676, A
25	21	US-10-719-900-909398	66.0	13.2	Sequence 909398, A
25	22	US-10-719-956-20800	66.0	13.2	Sequence 20800, A
25	22	US-10-719-956-141451	66.0	13.2	Sequence 141451, A
25	22	US-10-719-956-323250	66.0	13.2	Sequence 323250, A
25	22	US-10-719-956-463675	66.0	13.2	Sequence 463675, A
25	22	US-10-719-956-695450	66.0	13.2	Sequence 695450, A
25	24	US-11-036-317-28973	66.0	13.2	Sequence 28973, A
25	24	US-11-036-317-432467	66.0	13.2	Sequence 432467, A
25	24	US-11-036-317-637348	66.0	13.2	Sequence 637348, A
25	24	US-11-036-317-637349	66.0	13.2	Sequence 637349, A
50	18	US-10-682-595-9	65.0	13	Sequence 9, Appl1
25	21	US-10-719-900-331318	65.0	13	Sequence 331318, A
25	22	US-10-719-956-604675	64.0	12.8	Sequence 604675, A
21	20	US-10-751-736-54867	64.0	12.8	Sequence 54867, A
25	21	US-10-719-900-16121	64.0	12.8	Sequence 16121, A
25	21	US-10-719-900-23898	64.0	12.8	Sequence 23898, A
25	21	US-10-719-900-305562	64.0	12.8	Sequence 305562, A
25	21	US-10-719-900-308450	64.0	12.8	Sequence 308450, A
25	21	US-10-719-900-669161	64.0	12.8	Sequence 669161, A
25	21	US-10-809-189-124484	64.0	12.8	Sequence 124484, A
25	21	US-10-956-157-267755	64.0	12.8	Sequence 267755, A
25	22	US-10-843-527-65536	64.0	12.8	Sequence 65536, A
25	22	US-10-843-527-66018	64.0	12.8	Sequence 66018, A
25	22	US-10-843-527-172159	64.0	12.8	Sequence 172159, A
25	22	US-10-843-527-172641	64.0	12.8	Sequence 172641, A
25	22	US-10-719-956-342223	64.0	12.8	Sequence 342223, A
25	22	US-10-719-956-405841	64.0	12.8	Sequence 405841, A
25	24	US-11-036-317-688979	64.0	12.8	Sequence 688979, A
25	24	US-11-036-317-848656	64.0	12.8	Sequence 848656, A
25	14	US-10-215-112-759	63.0	12.6	Sequence 759, App
25	14	US-10-215-112-1650	63.0	12.6	Sequence 1650, Ap
25	15	US-10-098-263B-10873	63.0	12.6	Sequence 10873, A
25	15	US-10-098-263B-94994	63.0	12.6	Sequence 94994, A
25	21	US-10-719-900-17090	63.0	12.6	Sequence 17090, A
25	21	US-10-719-900-36690	63.0	12.6	Sequence 36690, A
25	21	US-10-719-900-65073	63.0	12.6	Sequence 65073, A
25	21	US-10-719-900-207353	63.0	12.6	Sequence 207353, A
25	21	US-10-719-900-285384	63.0	12.6	Sequence 285384, A
25	21	US-10-719-900-324618	63.0	12.6	Sequence 324618, A
25	21	US-10-719-900-326377	63.0	12.6	Sequence 326377, A
25	21	US-10-719-900-362460	63.0	12.6	Sequence 362460, A
25	21	US-10-719-900-366266	63.0	12.6	Sequence 366266, A
25	21	US-10-719-900-393795	63.0	12.6	Sequence 393795, A
25	21	US-10-719-900-408038	63.0	12.6	Sequence 408038, A
25	21	US-10-719-900-410842	63.0	12.6	Sequence 410842, A
25	21	US-10-719-900-428357	63.0	12.6	Sequence 428357, A
25	21	US-10-719-900-546950	63.0	12.6	Sequence 546950, A
25	21	US-10-719-900-546951	63.0	12.6	Sequence 546951, A
25	21	US-10-719-900-575400	63.0	12.6	Sequence 575400, A
25	21	US-10-719-900-602600	63.0	12.6	Sequence 602600, A
25	21	US-10-719-900-736492	63.0	12.6	Sequence 736492, A
25	21	US-10-719-900-764403	63.0	12.6	Sequence 764403, A
25	21	US-10-719-900-764692	63.0	12.6	Sequence 764692, A
25	21	US-10-719-900-806092	63.0	12.6	Sequence 806092, A
25	21	US-10-719-900-818073	63.0	12.6	Sequence 818073, A
25	21	US-10-719-900-914351	63.0	12.6	Sequence 914351, A

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:11:51 ; Search time 49.0476 Seconds  
(without alignments)  
667.220 Million cell updates/sec

Title: US-10-712-882A-2

Perfect score: 20

Sequence: 1 gtaccctccagatacatt 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:\*

- 1: /cgm2\_6/ptodata/1/ina/5A\_COMB.seq:\*
- 2: /cgm2\_6/ptodata/1/ina/5B\_COMB.seq:\*
- 3: /cgm2\_6/ptodata/1/ina/6A\_COMB.seq:\*
- 4: /cgm2\_6/ptodata/1/ina/6B\_COMB.seq:\*
- 5: /cgm2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
- 6: /cgm2\_6/ptodata/1/ina/backfiles.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	4	US-09-037-472-2
2	14.4	72.0	42	3	US-08-947-965-56
3	13.2	66.0	50	4	US-08-403-422-9
4	12.8	64.0	25	4	US-09-396-196G-124484
5	12.6	63.0	25	4	US-09-396-196G-76669
6	12.6	63.0	25	4	US-09-396-196G-93488
7	12.6	63.0	25	4	US-09-396-196G-93662
8	12.4	62.0	42	1	US-08-458-423A-25
9	12.4	62.0	42	1	US-08-458-424B-25
10	12.4	62.0	42	1	US-08-973-124-25
11	12.4	62.0	42	5	PCT-US96-08014-25
12	12.4	62.0	43	1	US-08-458-423A-26
13	12.4	62.0	43	1	US-08-458-424B-26
14	12.4	62.0	43	3	US-08-973-124-26
15	12.4	62.0	43	5	PCT-US96-08014-26
16	12.4	62.0	47	4	US-09-422-978-1150
17	12.2	61.0	25	4	US-09-396-196G-12687
18	12.2	61.0	25	4	US-09-396-196G-81164
19	12.2	61.0	30	1	US-07-947-683-15
20	12.2	61.0	30	1	US-08-400-323-18
21	12.2	61.0	38	4	US-09-474-432B-1219
22	12.2	61.0	38	4	US-09-476-387-1218
23	12.2	61.0	47	4	US-09-422-978-1944
24	12.0	60.0	21	4	US-09-973-180A-20
25	12	60.0	25	4	US-09-396-196G-92256
26	12	60.0	25	4	US-09-396-196G-105486
27	12	60.0	25	4	US-09-396-196G-105487

25	4	US-09-396-196G-105488	Sequence 105488, Appl
30	1	US-08-207-901-6	Sequence 6, Appl
37	4	US-09-589-462-5	Sequence 5, Appl
38	1	US-08-403-762A-55	Sequence 55, Appl
39	1	US-08-403-762A-54	Sequence 54, Appl
49	4	US-09-896-915-31	Sequence 31, Appl
50	2	US-09-060-828A-7	Sequence 7, Appl
50	2	US-09-060-828A-8	Sequence 8, Appl
25	4	US-09-396-196G-9873	Sequence 9873, Ap
25	4	US-09-396-196G-124485	Sequence 124485, Ap
31	1	US-08-061-889-7	Sequence 7, Appl
31	1	US-08-462-611-7	Sequence 7, Appl
31	3	US-08-623-428D-11	Sequence 11, Appl
31	5	PCT-US94-05378-7	Sequence 7, Appl
37	2	US-08-353-372A-33	Sequence 33, Appl
45	2	US-08-353-372A-34	Sequence 34, Appl
20	1	US-08-588-821-41	Sequence 41, Appl
20	1	US-08-915-214-41	Sequence 41, Appl
20	2	US-09-005-532-41	Sequence 41, Appl
20	4	US-09-198-452A-6451	Sequence 6451, Ap
24	2	US-08-687-080-122	Sequence 122, App
25	4	US-09-396-196G-21712	Sequence 21712, A
25	4	US-09-396-196G-73612	Sequence 73612, A
25	4	US-09-396-196G-93487	Sequence 93487, A
25	4	US-09-396-196G-93663	Sequence 93663, A
26	4	US-10-019-455A-2	Sequence 2, Appl
32	4	US-09-634-368-7	Sequence 7, Appl
44	4	US-08-401-192-10	Sequence 10, Appl
48	4	US-09-389-956-59	Sequence 59, Appl
25	3	US-09-396-196G-53785	Sequence 53785, A
20	3	US-09-326-186B-183	Sequence 183, App
22	4	US-09-447-349-7	Sequence 7, Appl
23	1	US-08-482-090-10	Sequence 10, Appl
23	2	US-09-007-383-12	Sequence 12, Appl
25	4	US-09-396-196G-2382	Sequence 2382, Ap
25	4	US-09-396-196G-19410	Sequence 19410, A
25	4	US-09-396-196G-44384	Sequence 44384, A
25	4	US-09-396-196G-44385	Sequence 44385, A
25	4	US-09-396-196G-73308	Sequence 73308, A
25	4	US-09-396-196G-84067	Sequence 84067, A
25	4	US-09-396-196G-84068	Sequence 84068, A
25	4	US-09-396-196G-84069	Sequence 84069, A
26	3	US-09-302-620B-55	Sequence 55, Appl
33	1	US-08-160-317-12	Sequence 12, Appl
33	1	US-08-351-147-12	Sequence 12, Appl
33	1	US-08-471-154-12	Sequence 12, Appl
33	1	US-08-629-600-10	Sequence 10, Appl
34	2	US-08-778-487-16	Sequence 16, Appl
34	3	US-08-891-516-16	Sequence 16, Appl
34	3	US-08-837-034-16	Sequence 16, Appl
42	2	US-08-343-443B-58	Sequence 58, Appl
45	1	US-08-171-389-33	Sequence 33, Appl
45	1	US-08-123-936-33	Sequence 33, Appl
45	2	US-08-475-228A-33	Sequence 33, Appl
45	3	US-08-482-080A-33	Sequence 33, Appl
45	3	US-09-354-947-33	Sequence 33, Appl
45	5	PCT-US93-12388-33	Sequence 33, Appl
47	4	US-09-422-978-1086	Sequence 1086, Ap
47	4	US-09-422-978-1738	Sequence 1738, Ap
47	4	US-09-422-978-1805	Sequence 1805, Ap
47	4	US-09-422-978-1964	Sequence 1964, Ap
17	3	US-09-360-416-7	Sequence 7, Appl
23	3	US-09-157-177-81	Sequence 81, Appl
23	3	US-09-157-177-99	Sequence 99, Appl
23	4	US-09-541-210-81	Sequence 81, Appl
23	4	US-09-541-210-99	Sequence 99, Appl
25	1	US-08-433-126A-131	Sequence 131, App
25	1	US-08-433-124A-131	Sequence 131, App
25	3	US-08-952-670-7	Sequence 7, Appl
25	3	US-08-976-413A-131	Sequence 131, App
25	4	US-09-396-196G-6592	Sequence 6592, Ap
25	4	US-09-396-196G-10019	Sequence 10019, A
25	4	US-09-396-196G-10020	Sequence 10020, A

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:46:26 ; Search time 1296.76 Seconds  
(without alignments)  
587.066 Million cell updates/sec

Title: US-10-712-882A-2

Perfect score: 20

Sequence: 1 gtaccttcgagatacatt 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_est4:\*

5: gb\_est5:\*

6: gb\_est6:\*

7: gb\_est7:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	14.8	74.0	33	8	AZ819756
2	13.8	69.0	38	8	BH855957
3	12.6	63.0	28	8	AZ412849
4	12.6	63.0	40	9	HA275800
5	12.2	61.0	45	1	AJ789878
6	12.2	61.0	50	9	TA197A12Q
7	12.0	60.0	42	9	EX206184
8	12.0	60.0	47	8	BH846317
9	12.0	60.0	47	9	EX947538
10	12.0	60.0	48	8	AZ946178
11	11.8	59.0	46	9	AL757972
12	11.8	59.0	47	9	TA67C12Q
13	11.8	59.0	48	8	BH789937
14	11.8	59.0	50	8	AZ621023
15	11.6	58.0	30	7	CO782579
16	11.6	58.0	30	9	AG204185
17	11.6	58.0	31	8	AZ585462
18	11.6	58.0	32	8	AZ809367
19	11.6	58.0	36	2	AW250732
20	11.6	58.0	37	7	D18713
21	11.6	58.0	39	9	EX896780
22	11.4	57.0	40	9	BSMC16708
23	11.4	57.0	48	5	BW590884
24	11.4	57.0	50	7	CN749028

25	11.2	56.0	21	9	CL676658
26	11.2	56.0	29	9	CL657998
27	11.2	56.0	39	8	AZ785706
28	11.2	56.0	42	1	AU256554
29	11.2	56.0	42	8	AZ784009
30	11.2	56.0	45	9	CR404033
31	11.2	56.0	46	8	AZ440102
32	11.2	56.0	46	8	BH791712
33	11.1	55.0	34	1	AU256421
34	11.1	55.0	34	7	R96723
35	11.1	55.0	36	8	AZ925959
36	11.1	55.0	37	9	AZ37C10P
37	11.1	55.0	37	9	CR399334
38	11.1	55.0	44	9	AI431480
39	11.1	55.0	46	1	AI041460
40	11.1	55.0	49	1	AZ332306
41	11.1	55.0	50	8	BH855636
42	10.8	54.0	50	8	AZ347672
43	10.8	54.0	29	8	AL768125
44	10.8	54.0	30	9	AZ375068
45	10.8	54.0	43	1	AI004480
46	10.8	54.0	46	1	BJ045167
47	10.8	54.0	49	9	CC886568
48	10.8	54.0	50	2	BE978444
49	10.6	53.0	28	1	AI174152
50	10.6	53.0	28	1	AI429345
51	10.6	53.0	30	9	EX947818
52	10.6	53.0	30	9	TA383B12P
53	10.6	53.0	31	9	AL760797
54	10.6	53.0	34	2	BE257894
55	10.6	53.0	35	9	TA306A02P
56	10.6	53.0	38	9	AY127102
57	10.6	53.0	39	2	BE512831
58	10.6	53.0	39	9	CC796849
59	10.6	53.0	41	9	CG804184
60	10.6	53.0	42	8	BH911098
61	10.6	53.0	43	7	D67705
62	10.6	53.0	45	2	BE267956
63	10.6	53.0	45	2	BE513871
64	10.6	53.0	45	2	BE560611
65	10.6	53.0	46	2	BE367872
66	10.6	53.0	47	2	BE267896
67	10.6	53.0	47	2	BE270087
68	10.6	53.0	47	2	BE295974
69	10.6	53.0	47	2	BE513247
70	10.6	53.0	47	2	BE561502
71	10.6	53.0	47	8	BZ358986
72	10.6	53.0	47	9	EX534569
73	10.6	53.0	48	6	CD568311
74	10.6	53.0	49	1	AI629210
75	10.6	53.0	49	1	AI784643
76	10.6	53.0	49	2	BE397307
77	10.6	53.0	49	8	AZ596631
78	10.4	52.0	23	1	AJ801164
79	10.4	52.0	24	8	AZ345622
80	10.4	52.0	25	7	H50411
81	10.4	52.0	25	9	CG718660
82	10.4	52.0	29	8	AZ507569
83	10.4	52.0	30	9	AL759103
84	10.4	52.0	31	9	CG718776
85	10.4	52.0	36	2	BE868589
86	10.4	52.0	37	1	CG179523
87	10.4	52.0	37	9	AI720308
88	10.4	52.0	39	8	BH853386
89	10.4	52.0	41	8	BH855694
90	10.4	52.0	41	9	CG718657
91	10.4	52.0	43	1	AA230136
92	10.4	52.0	43	1	AA509591
93	10.4	52.0	43	8	AZ788733
94	10.4	52.0	43	8	BH865613
95	10.4	52.0	43	8	BZ765761
96	10.4	52.0	43	9	CG718551
97	10.4	52.0	43	9	CG730127

CL676658	PR10119b-
CL657998	PR10130a-
AZ785706	2M0029C23
AU256554	AU256554
AZ784009	2M0026G16
CR404033	ArabiDops
AZ440102	IM0231F06
BH791712	SALK_0609
AU256421	AU256421
R96723	YQ55B09_81
AZ925959	476_dio05
AZ37C10P	T_brucei
CR399334	ArabiDops
AI431480	th40F03.X
AI041460	ow36D07.S
AZ332306	IM0060B18
BH855636	SALK_0848
AZ347672	IM0083C21
AL768125	ArabiDops
AZ375068	IM0128E15
AI004480	ot56G05.S
BJ045167	BJ045167
CC886568	SALK_1487
BE978444	BS75H03.Y
AI174152	vz84D07.I
AI429345	mn95C09.X
EX947818	ArabiDops
AL498156	T_brucei
AL760797	ArabiDops
BE257894	601109491
AY127102	T_brucei
BE512831	601171854
CC796849	SALK_1441
CG804184	1118048C0
BH911098	SALK_0651
D67705	CELK076G4F
BE267956	601125354
BE513871	601316443
BE560611	601345809
BE267872	601125422
BE267896	601125461
BE270087	601185780
BE295974	601174272
BE513247	601353076
BE561502	601346576
BZ358986	SALK_1336
EX534569	ArabiDops
CD568311	04H23a Ar
AI629210	fc04h06.Y
AI784643	ta03b10.X
BE397307	601288639
AZ596631	IM0410F06
AJ801164	AJ801164
AZ345622	IM0080F20
H50411	yo29a12.S1
CG718660	1119054A0
AZ507569	IM0349G13
AL759103	ArabiDops
CG718776	1119054D1
BE868589	601445552
CG179523	1119058A0
AI720308	as57D01.X
BH853386	SALK_0769
BH855694	SALK_0847
CG718657	1119054A0
AA230136	nc37a05.I
AA509591	vf85D01.I
AZ788733	2M0036M03
BH865613	SALK_0990
BZ765761	SALK_1342
CG718551	1119053E0
CG730127	1119119E0

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 16:54:30 ; Search time 173.048 Seconds  
(without alignments)  
684.175 Million cell updates/sec

Title: US-10-712-882A-2

Perfect score: 20

Sequence: 1 gtaccttcgagatacatt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N Geneseq 16Dec04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	Aav32390 Interleuk
2	14.2	71.0	25	9	AC110883 Human mic
3	14.2	71.0	30	3	Aaz290468 Mutated N
4	14.2	71.0	30	3	Aaz290469 Mutated N
5	13.2	66.0	25	9	AC194931 Human mic
6	13.2	66.0	25	9	AC194930 Human mic
7	13.2	66.0	31	3	AAA79121 Human gen
8	13.2	66.0	32	4	AAD13154 Human WTS
9	13.2	66.0	50	2	AAV71989 Human com
10	12.8	64.0	24	6	ABV73430 Mouse cla
11	12.8	64.0	36	3	AAA39713 S. lemnae
12	12.8	64.0	36	3	AAA39712 S. lemnae
13	12.8	64.0	40	2	AAT70794 Stenotic
14	12.8	64.0	43	10	ADC38618 MLL-AP4 f
15	12.6	63.0	25	9	AC110882 Human mic
16	12.6	63.0	25	9	AC195003 Human mic
17	12.6	63.0	25	9	ACH51623 DNA targe
18	12.6	63.0	25	9	ACH52514 DNA targe
19	12.6	63.0	28	12	ADI47233 Enterococ
20	12.6	63.0	31	10	ADG42318 Fatty alc

C	21	12.6	63.0	33	6	ABL55522	ABL5522 Human MAM
C	22	12.6	63.0	35	10	ADG37066	Adg37066 Human ubi
C	23	12.6	63.0	43	6	ABZ26856	Abz26856 Candida e
C	24	12.6	63.0	50	6	ABZ04090	Abz04090 Human leu
C	25	12.6	63.0	50	12	ADP10051	Adp10051 50-mer ol
C	26	12.6	63.0	50	12	ADP09996	Adp09996 50-mer ol
C	27	12.4	62.0	21	6	ABK65557	Abk65557 Human sin
C	28	12.4	62.0	25	9	AC177807	Ac177807 Human mic
C	29	12.4	62.0	25	9	AC102616	Ac102616 Human mic
C	30	12.4	62.0	25	9	AC152277	Ac152277 Human mic
C	31	12.4	62.0	25	12	ADP13746	Adp13746 Renal cel
C	32	12.4	62.0	31	3	AAA78896	Aaa78896 Human gen
C	33	12.4	62.0	42	2	AAT65167	Aat65167 Transform
C	34	12.4	62.0	43	2	AAT65168	Aat65168 Transform
C	35	12.4	62.0	47	3	AAZ66803	Aaz66803 Human map
C	36	12.2	61.0	21	8	ABX70518	Abx70518 PCR prime
C	37	12.2	61.0	21	8	ABX70515	Abx70515 PCR prime
C	38	12.2	61.0	21	12	ADL24167	Adl24167 Human NOV
C	39	12.2	61.0	21	12	ADL24170	Adl24170 Human NOV
C	40	12.2	61.0	25	9	AC107436	Ac107436 Human mic
C	41	12.2	61.0	25	9	AC182921	Ac182921 Human mic
C	42	12.2	61.0	25	9	AC144741	Ac144741 Human mic
C	43	12.2	61.0	25	9	AC118059	Ac118059 Human mic
C	44	12.2	61.0	25	9	AC146971	Ac146971 Human mic
C	45	12.2	61.0	25	9	AC182920	Ac182920 Human mic
C	46	12.2	61.0	25	9	ACH59525	Ach59525 DNA targe
C	47	12.2	61.0	25	9	ACH54010	Ach54010 DNA targe
C	48	12.2	61.0	27	6	ABN83410	Abn83410 Mutant TE
C	49	12.2	61.0	27	6	ABN83418	Abn83418 Mutant TE
C	50	12.2	61.0	27	6	ABN83403	Abn83403 Mutant TE
C	51	12.2	61.0	27	6	ABN83419	Abn83419 Mutant TE
C	52	12.2	61.0	27	6	ABN83397	Abn83397 Wild-type
C	53	12.2	61.0	27	6	ABN83399	Abn83399 Mutant TE
C	54	12.2	61.0	27	6	ABN83411	Abn83411 Mutant TE
C	55	12.2	61.0	30	2	AAT63287	Aat63287 Probe for
C	56	12.2	61.0	30	2	AAV05503	Aav05503 Probe for
C	57	12.2	61.0	31	2	AAK06463	Aak06463 Human bia
C	58	12.2	61.0	32	3	ABL60008	AbL60008 Saccharom
C	59	12.2	61.0	33	6	ABA04810	AbA04810 Ligase co
C	60	12.2	61.0	33	6	AAI42571	Aai42571 Phospholi
C	61	12.2	61.0	33	12	ADO11216	Ado11216 Single mu
C	62	12.2	61.0	33	12	ADO11165	Ado11165 Single mu
C	63	12.2	61.0	35	12	ADO18941	Ado18941 Sequence
C	64	12.2	61.0	38	2	AAQ13108	Aaq13108 TAG seque
C	65	12.2	61.0	38	6	ABL54535	AbL54535 Pectinatu
C	66	12.2	61.0	38	8	ACD53874	AcD53874 HBV zinzy
C	67	12.2	61.0	38	12	ADM62245	Adm62245 Hepatitis
C	68	12.2	61.0	39	10	ADC81588	Adc81588 Murine PG
C	69	12.2	61.0	40	10	ADC81589	Adc81589 Modified
C	70	12.2	61.0	47	3	AAZ67597	Aaz67597 Human map
C	71	12	60.0	21	13	ABZ69338	Abz69338 Human SIC
C	72	12	60.0	21	13	ADSL17266	Adsl17266 Murine in
C	73	12	60.0	24	10	ABS57684	Abs57684 P. falcip
C	74	12	60.0	25	9	AC161233	Ac161233 Human mic
C	75	12	60.0	25	9	AC167985	Ac167985 Human mic
C	76	12	60.0	25	9	AC172627	Ac172627 Human mic
C	77	12	60.0	30	1	AAAN91917	Aaan91917 5'-portio
C	78	12	60.0	30	2	AAQ13598	Aaq13598 5' portio
C	79	12	60.0	30	2	AAT74346	Aat74346 5' end of
C	80	12	60.0	33	12	ADQ76254	Adq76254 Bacillus
C	81	12	60.0	37	4	AAAC92053	Aac92053 Human PBR
C	82	12	60.0	37	10	ADC72983	Adc72983 Forward P
C	83	12	60.0	38	2	AAQ84433	Aaq84433 Mycobacte
C	84	12	60.0	39	2	AAQ84432	Aaq84432 Mycobacte
C	85	12	60.0	47	4	AAI74326	Aai74326 Human eil
C	86	12	60.0	49	3	AAAS9289	Aas9289 Nucleotid
C	87	12	60.0	50	13	ADS91763	Ads91763 Nematode
C	88	11.8	59.0	17	6	ABV79754	Abv79754 Human HTP
C	89	11.8	59.0	17	6	ABV79753	Abv79753 Human HTP
C	90	11.8	59.0	17	6	ABV79752	Abv79752 Human HTP
C	91	11.8	59.0	18	8	ABZ10993	Abz10993 Haematopo
C	92	11.8	59.0	19	6	ABZ38506	Abz38506 Bovine le
C	93	11.8	59.0	22	8	ABV74591	Abv74591 Human per

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:41:56 ; Search time 694.476 Seconds  
(without alignments)  
1395.446 Million cell updates/sec

Title: US-10-712-882A-2  
Perfect score: 20  
Sequence: 1 gtacottccagatatacatt 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	6	AR490510 Sequence
2	14.4	72.0	42	6	AR095597 Sequence
3	13.2	66.0	31	6	BD002825 Gene comp
C 4	13.2	66.0	46	1	ECOSERNA
C 5	13.2	66.0	50	6	M16640 E. coli 5'-t
C 6	13.2	66.0	50	6	AR451821 Sequence
7	12.6	63.0	28	6	BD084653 Human com
8	12.6	63.0	43	6	CQ765858 Sequence
9	12.6	63.0	50	6	AX483435 Sequence
C 10	12.4	62.0	31	6	BD002600 Gene comp
11	12.4	62.0	42	6	AR140748 Sequence
12	12.4	62.0	42	6	193427 Sequence
13	12.4	62.0	42	6	I95054 Sequence
14	12.4	62.0	43	6	AR140749 Sequence
15	12.4	62.0	43	6	193428 Sequence
16	12.4	62.0	43	6	195055 Sequence
C 17	12.4	62.0	47	6	AR289415 Sequence
C 18	12.2	61.0	27	6	AX452277 Sequence
C 19	12.2	61.0	27	6	AX452279 Sequence

C 20	12.2	61.0	27	6	AX452283 Sequence
C 21	12.2	61.0	27	6	AX452290 Sequence
C 22	12.2	61.0	27	6	AX452291 Sequence
C 23	12.2	61.0	27	6	AX452298 Sequence
C 24	12.2	61.0	27	6	AX452299 Sequence
25	12.2	61.0	30	6	I32954 Sequence 15
26	12.2	61.0	30	6	I87104 Sequence 18
27	12.2	61.0	31	11	CR383624 Arabidops
28	12.2	61.0	33	6	BD167771 Novel PLA
C 29	12.2	61.0	38	6	AR286847 Sequence
C 30	12.2	61.0	38	6	AR398837 Sequence
C 31	12.2	61.0	38	6	BD107569 Nucleic a
C 32	12.2	61.0	39	6	AX839149 Sequence
C 33	12.2	61.0	40	6	AX839150 Sequence
C 34	12.2	61.0	41	6	AX514677 Sequence
C 35	12.2	61.0	41	6	AX520617 Sequence
36	12.2	61.0	47	6	AR290209 Sequence
37	12	60.0	30	6	I42193 Sequence 6
38	12	60.0	30	6	BD014140 Probe for
39	12	60.0	34	6	CQ875106 Sequence
C 40	12	60.0	34	6	AX057571 Sequence
C 41	12	60.0	37	6	AR308526 Sequence
42	12	60.0	38	6	A42723 Sequence 55
43	12	60.0	38	6	I87229 Sequence 55
44	12	60.0	39	6	A42722 Sequence 54
45	12	60.0	39	6	I87228 Sequence 54
C 46	12	60.0	47	6	AX157939 Sequence
47	12	60.0	49	6	BD237845 Optical s
48	12	60.0	49	6	AX026790 Sequence
49	12	60.0	50	6	AR084823 Sequence
C 50	12	60.0	50	6	AR084824 Sequence
51	11.8	59.0	17	6	AX499691 Sequence
52	11.8	59.0	17	6	AX499692 Sequence
53	11.8	59.0	17	6	AX499693 Sequence
C 54	11.8	59.0	18	6	AX599793 Sequence
55	11.8	59.0	22	6	BD178409 Novel clo
56	11.8	59.0	25	6	AX501688 Sequence
57	11.8	59.0	25	6	AX501689 Sequence
58	11.8	59.0	25	6	AX501690 Sequence
59	11.8	59.0	25	6	AX501691 Sequence
60	11.8	59.0	25	6	AX501692 Sequence
61	11.8	59.0	25	6	AX501693 Sequence
62	11.8	59.0	25	6	AX501694 Sequence
63	11.8	59.0	25	6	AX501695 Sequence
64	11.8	59.0	25	6	AX501696 Sequence
65	11.8	59.0	25	6	AX501697 Sequence
66	11.8	59.0	25	6	AX501698 Sequence
C 67	11.8	59.0	30	6	A33413 Synthetic p
C 68	11.8	59.0	31	6	AR176494 Sequence 7
C 69	11.8	59.0	31	6	I59460 Sequence 7
C 70	11.8	59.0	34	6	A33412 Synthetic p
C 71	11.8	59.0	37	6	AR059413 Sequence
C 72	11.8	59.0	45	6	AR059414 Sequence
C 73	11.8	59.0	48	6	AX583326 Sequence
C 74	11.6	58.0	20	6	AR043253 Sequence
C 75	11.6	58.0	20	6	AR074908 Sequence 41
C 76	11.6	58.0	20	6	I82104 Sequence 41
C 77	11.6	58.0	20	6	AR315914 Sequence
C 78	11.6	58.0	20	6	BD082862 Reagents
79	11.6	58.0	21	6	CQ788005 Sequence
C 80	11.6	58.0	24	6	AR079331 Sequence
C 81	11.6	58.0	24	6	CQ816703 Sequence
C 82	11.6	58.0	24	6	BD094567 Substrate
C 83	11.6	58.0	26	6	BD010801 Novel pol
C 84	11.6	58.0	26	6	BD093102 Novel pol
C 85	11.6	58.0	28	6	BD267784 Potenti
C 86	11.6	58.0	28	6	BD267818 Enhanceme
C 87	11.6	58.0	29	6	AX721999 Sequence
C 88	11.6	58.0	30	6	CQ816721 Sequence
C 89	11.6	58.0	32	6	AR393791 Sequence
C 90	11.6	58.0	32	6	AX084109 Sequence
C 91	11.6	58.0	33	6	AX235239 Sequence
C 92	11.6	58.0	36	6	CQ847567 Sequence

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:30:35 ; Search time 413.229 Seconds  
(without alignments)  
455.077 Million cell updates/sec

Title: US-10-712-882A-1

Perfect score: 27

Sequence: 1 aagctgtttaccactgaactagc 27

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 10399348

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications NA: \*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	10	US-09-888-056A-5
2	27	100.0	27	15	US-10-167-127-29
3	27	100.0	27	16	US-10-172-919-13
4	27	100.0	27	20	US-10-823-197-13
5	27	100.0	27	21	US-10-712-882-1
6	27	100.0	27	21	US-10-712-882-9
7	27	100.0	27	21	US-10-838-503-15
Sequence 5, Appl1					
Sequence 29, Appl					
Sequence 13, Appl					
Sequence 13, Appl					
Sequence 1, Appl					
Sequence 9, Appl					
Sequence 15, Appl					

Sequence 7, Appl1	22	81.5	22	US-10-712-882-7	21	US-10-712-882-7	Sequence 7, Appl1
Sequence 12, Appl	21	77.8	21	US-09-845-129-12	21	US-10-802-061-12	Sequence 12, Appl
Sequence 118759,	25	62.2	25	US-10-098-263B-118759	25	US-10-098-263B-118759	Sequence 118759,
Sequence 877295,	25	61.5	25	US-10-719-900-877295	25	US-10-719-900-877295	Sequence 877295,
Sequence 2940, Ap	47	60.7	47	US-10-349-143-2940	47	US-10-349-143-2940	Sequence 2940, Ap
Sequence 8751, Ap	25	60.0	25	US-10-681-773-8751	25	US-10-681-773-8751	Sequence 8751, Ap
Sequence 87674, A	25	60.0	25	US-10-719-900-500286	25	US-10-719-900-500286	Sequence 87674, A
Sequence 501286,	25	59.3	25	US-10-719-956-401736	25	US-10-719-956-401736	Sequence 501286,
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Total number of hits satisfying chosen parameters: 1209694

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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5	27	100.0	27	4	US-09-632-657-15
6	27	100.0	27	4	US-09-693-555A-17
7	27	100.0	27	4	US-09-594-950-17
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10	22	81.5	22	4	US-09-037-472-7
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12	22	81.5	22	5	PCT-US96-12455-1
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14	21	77.8	21	4	US-09-845-129-12
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16	15.8	58.5	47	4	US-09-422-978-1413
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21	14.4	53.3	44	6	5498600-32
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Post-processing: Minimum Match 0%  
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Listing first 100 summaries

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62	11.8	43.7	40	1	AA452048
63	11.8	43.7	41	8	BH641362
64	11.8	43.7	42	4	BG682762
65	11.8	43.7	44	8	BX184327
66	11.8	43.7	44	8	BZ356371
67	11.8	43.7	45	8	AZ480534
68	11.8	43.7	45	8	AZ769358
69	11.8	43.7	47	8	BZ763663
70	11.8	43.7	49	2	AV965281
71	11.8	43.7	50	1	AU104852
72	11.8	43.7	50	1	AU104853
73	11.8	43.7	50	1	AU104855
74	11.8	43.7	50	4	BG408716
75	11.8	43.7	50	8	AZ635616
76	11.8	43.7	50	9	CR129418
77	11.6	43.0	25	8	AZ871751
78	11.6	43.0	34	8	AZ619032
79	11.6	43.0	37	8	BZ593763
80	11.6	43.0	45	1	AA794942
81	11.6	43.0	45	9	BX948798
82	11.6	43.0	45	9	CG846879
83	11.6	43.0	46	4	BU039761
84	11.6	43.0	48	1	AU243906
85	11.6	43.0	48	6	CD746731
86	11.6	43.0	49	1	AA673527
87	11.6	43.0	49	8	AZ773638
88	11.6	43.0	49	9	BX178350
89	11.6	43.0	50	1	AU105749
90	11.6	43.0	50	1	AU107351
91	11.6	43.0	50	1	AU107686
92	11.6	43.0	50	1	AU107688
93	11.6	43.0	50	8	AZ921893
94	11.4	42.2	20	8	AZ792320
95	11.4	42.2	23	9	AG188248
96	11.4	42.2	29	8	BH848482
97	11.4	42.2	29	8	BZ381738

AZ396226	IM0160N09
AZ504924	IM0345B23
AZ627990	IM0476A08
AZ576414	AST-2T009
CG783331	01S0530-0
U21495	U21495
BX660493	Arabidops
AU254169	AU254169
BO585750	E011419-0
CC458729	SALK_1217
AI583675	tt74H06.x
AZ474111	IM0290F22
AZ411075	IM0184B06
BZ380513	SALK_1152
AI636188	tz06E08.x
AZ783979	2M0026K08
AJ593815	Arabidops
AU103054	AU103054
CN973588	21092_60-
CO730398	ShESTba2
CR203941	Forward s
AZ434231	IM0220H03
BZ595231	SALK_0863
AA689975	vq10A06.t
AI174397	an41C09.8
AQ025245	EP (3) 3062
AI282047	GG88F07.x
BH906956	SALK_0368
AA116551	tm27F03.x
AI762609	w156D08.x
AV968446	AV968446
CC516471	CH240_362
AZ827644	2M0104N08
CG717990	1119051B1
AZ812736	2M0079E09
AZ615836	IM0445D21
CC053460	SALK_0435
AA452048	xx12E05.t
BH641362	1008047A0
BG682762	602830285
BX184327	Danio rer
BZ356371	SALK_1288
AZ480534	IM0302E07
AZ769358	IM0569M20
BZ763663	SALK_1201
AV965281	AV965281
AU104852	AU104852
AU104853	AU104853
AU104855	AU104855
BG408716	gb77E07.Y
AZ635616	IM0493C18
CR129418	Reverte.8
AZ871751	2M0184116
AZ619032	IM0451K07
BZ593763	SALK_0820
AA794942	vr05G03..x
BX948798	Arabidops
CG846879	01S0536-0
BU039761	BU039761
AU243906	AU243906
CD746731	S203_B06
AA673527	35736F10.t
AZ773638	2M0001010
BX178350	Danio rer
AU105749	AU105749
AU107351	AU107351
AU107686	AU107686
AU107688	AU107688
AZ921893	HRC0C3D04
AZ792320	2M0043N09
AG188248	Pan trogl
BH848482	SALK_0684
BZ381738	SALK_1171



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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 16:54:30 ; Search time 233.614 Seconds  
(without alignments)  
684.175 Million cell updates/sec

Title: US-10-712-882A-1

Perfect score: 27  
Sequence: 1 agctgtgtctaccactgaactagc 27

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : N Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	27	100.0	27	2	Aav32389 Interleuk
2	27	100.0	27	2	Aaz10700 PCR prime
3	27	100.0	27	2	Aax75921 Human int
4	27	100.0	27	3	Aaz37218 PCR prime
5	27	100.0	27	3	Aac63004 Human IL-
6	27	100.0	27	5	Aac91431 Human IL-
7	27	100.0	27	6	Aad27381 PCR prime
8	27	100.0	27	8	Aal54507 Ageing-re
9	27	100.0	27	10	AAD51461 Human int
10	27	100.0	27	12	ADL83335 PCR prime
11	27	100.0	27	12	ADN48852 Human int
12	27	100.0	27	12	ADQ35280 Human int
13	22	81.5	22	2	AAT70316 Primer fo
14	22	81.5	22	3	Aaz37202 PCR prime
15	22	81.5	22	3	Aac63024 Human IL-
16	21	77.8	21	2	AAX16611 Interleuk
17	21	77.8	21	2	ABX15539 Human IL-
18	21	77.8	21	4	Aaf27676 Primer #9
19	16.8	62.2	25	9	ACK18778 Human mic
20	16.4	60.7	47	3	Aaz68591 Human map

c	21	15.8	58.5	47	3	Aaz67066	Aaz67066 Human map
c	22	15.2	56.3	25	9	ACK18779	ACK18779 Human mic
c	23	14.8	54.8	20	2	AAQ28501	AAQ28501 Polymeras
c	24	14.8	54.8	45	3	AAA51868	AAA51868 Primer fo
c	25	14.6	54.1	25	9	ACI78440	ACI78440 Human mic
c	26	14.6	54.1	25	9	ACI77838	ACI77838 Human mic
c	27	14.6	54.1	42	12	ADM36323	Adm36323 Bacteriop
c	28	14.4	53.3	32	6	ABS52892	ABe52892 N-acetylgl
c	29	14.4	53.3	39	2	AAT61460	Aat61460 5' primer
c	30	14.2	52.6	19	2	AAV32395	AAV32395 Interleuk
c	31	14.2	52.6	25	9	ACI87658	ACI87658 Human mic
c	32	14.2	52.6	30	3	AAA73108	AAa73108 Human MCl
c	33	14.2	52.6	31	13	ADR73576	Adr73576 Staphyloc
c	34	14.2	52.6	35	4	AAD20650	Aad20650 Salmonell
c	35	14.2	52.6	35	9	AAI56578	AAI56578 PCR prime
c	36	14.2	52.6	38	4	AAF76985	AAf76985 Human G p
c	37	14.2	52.6	41	4	AAI66442	AAi66442 DBH and p
c	38	14.2	52.6	41	12	ADKL7885	Adk17885 Cytochrom
c	39	14.2	52.6	50	4	AAU32458	AAI32458 Human SNP
c	40	14	51.9	25	9	ACH56236	Ach56236 DNA targe
c	41	14	51.9	33	6	ABV75444	ABv75444 Human tra
c	42	14	51.9	41	6	ABZ44028	ABz44028 Human NDU
c	43	14	51.9	41	6	ABZ49972	ABz49972 Human NDU
c	44	14	51.9	42	3	AAZ29543	AAa29543 Codon alt
c	45	14	51.9	45	3	AAZ58474	AAz58474 Human PRO
c	46	13.8	51.1	19	2	AAT96922	Aat96922 Human pRB
c	47	13.8	51.1	25	9	ACK20090	ACK20090 Human mic
c	48	13.8	51.1	25	9	ACI57422	ACi57422 Human mic
c	49	13.8	51.1	25	9	ACI95662	ACi95662 Human mic
c	50	13.8	51.1	25	9	ACI95663	ACi95663 Human mic
c	51	13.8	51.1	25	9	ACK03316	ACK03316 Human mic
c	52	13.8	51.1	25	9	ACK02690	ACK02690 Human mic
c	53	13.8	51.1	25	9	ACK20726	ACK20726 Human mic
c	54	13.8	51.1	28	12	ADQ14756	Adq14756 Nfa-speci
c	55	13.8	51.1	29	2	AAQ66652	AAq66652 PCR prime
c	56	13.8	51.1	29	12	ADH23241	Adh23241 Stenotro
c	57	13.8	51.1	31	3	AAAF79198	AAa79198 Human gen
c	58	13.8	51.1	41	5	AAF62022	AAf62022 Canine IL
c	59	13.8	51.1	41	11	ADP71353	Adp71353 Primer #1
c	60	13.8	51.1	41	11	ADP71354	Adp71354 Primer #2
c	61	13.8	51.1	48	13	ADQ89899	Adq89899 Primer of
c	62	13.8	51.1	50	4	AAI34269	AAI34269 Human SNP
c	63	13.8	51.1	50	12	ADF93983	Adf93983 Microorga
c	64	13.8	51.1	50	12	ADF94012	Adf94012 Microorga
c	65	13.8	51.1	50	12	ADF94015	Adf94015 Microorga
c	66	13.6	50.4	20	6	AAI72107	AAi72107 PGI-VPR f
c	67	13.6	50.4	23	12	ADJ57664	Adj57664 Primer of
c	68	13.6	50.4	25	3	AAA92094	AAa92094 Human Lhx
c	69	13.6	50.4	25	3	AAA92093	AAa92093 Human Lhx
c	70	13.6	50.4	33	6	ABL54229	ABl54229 Human G-p
c	71	13.6	50.4	43	12	ADP97095	Adp97095 C. albica
c	72	13.6	50.4	46	10	ADD94287	Ada94287 Mouse HUI
c	73	13.6	50.4	50	6	ABZ07241	ABz07241 Human leu
c	74	13.4	49.6	21	10	ADM14293	Adm14293 Human src
c	75	13.4	49.6	21	10	ADM10351	Adm10351 Human CYP
c	76	13.4	49.6	23	12	ADO25213	Ado25213 E. coli g
c	77	13.4	49.6	24	6	ABZ31657	ABz31657 Candida a
c	78	13.4	49.6	25	9	ACI63490	ACi63490 Human mic
c	79	13.4	49.6	25	9	ACI97672	ACi97672 Human mic
c	80	13.4	49.6	25	10	ADJ87874	Adj87874 G-coupled
c	81	13.4	49.6	28	12	ADO56055	Ado56055 Human NOV
c	82	13.4	49.6	28	2	AAV26909	AAv26909 PHO3 gene
c	83	13.4	49.6	28	4	AAZ27377	AAz27377 Yeast Pho
c	84	13.4	49.6	29	8	AAD49058	AAa49058 Saprolegn
c	85	13.4	49.6	29	12	ADK60325	Adk60325 Angiogene
c	86	13.4	49.6	29	12	ADK60626	Adk60626 Angiogene
c	87	13.4	49.6	29	12	ADP73249	Adp73249 Primer of
c	88	13.4	49.6	31	12	ADIO3839	Adi03839 PCR prime
c	89	13.4	49.6	32	8	AAI52203	AAI52203 Human ret
c	90	13.4	49.6	32	12	ADIO3845	Adi03845 PCR prime
c	91	13.4	49.6	32	12	ADIO3841	Adi03841 PCR prime
c	92	13.4	49.6	32	12	ADIO3843	Adi03843 PCR prime
c	93	13.4	49.6	35	4	AAD20651	Aad20651 Salmonell

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 18:41:56 ; Search time 937.543 Seconds  
(without alignments)  
1395.446 Million cell updates/sec

Title: US-10-712-882A-1

Perfect score: 27  
Sequence: 1 aagctgttctaccactgaactagc 27

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database: GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_scs.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	27	6	AR112236 Sequence
2	27	100.0	27	6	AR490509 Sequence
3	27	100.0	27	6	AR490517 Sequence
4	27	100.0	27	6	AR493820 Sequence
5	27	100.0	27	6	AR532952 Sequence
6	27	100.0	27	6	AR534190 Sequence
7	27	100.0	27	6	AR542781 Sequence
8	27	100.0	27	6	AX012487 Sequence
9	27	100.0	27	6	AX052803 Sequence
10	27	100.0	27	6	AX360019 Sequence
11	27	100.0	27	6	BD085845 Methods
12	22	81.5	22	6	AR112256 Sequence
13	22	81.5	22	6	I73225 Sequence 1
14	22	81.5	22	6	AR490515 Sequence
15	22	81.5	22	6	AR534174 Sequence
16	21	77.8	21	6	A82467 Sequence 5
17	21	77.8	21	6	AR487075 Sequence
18	21	77.8	21	6	AX067276 Sequence
19	21	77.8	21	6	BD124528 Predictio

20	16.4	60.7	45	6	AX027655	Sequence
21	16.4	60.7	47	6	AR291205	Sequence
22	15.8	58.5	47	6	AR289678	Sequence
23	15.6	57.8	39	6	AR050328	Sequence
24	14.8	54.8	20	6	I13552	Sequence 2
25	14.4	53.3	32	6	BD166382	DNA encod
26	14.4	53.3	39	6	E12937	Sequence
27	14.4	53.3	44	6	AR365487	Sequence
28	14.4	53.3	49	4	FCLTRNA	Sequence
29	14.2	52.6	28	6	CQ794117	Sequence
30	14.2	52.6	28	6	CQ800086	Sequence
31	14.2	52.6	30	6	E36185	Upstream re
32	14.2	52.6	35	6	AX254701	Sequence
33	14.2	52.6	35	6	AX766357	Sequence
34	14.2	52.6	38	6	BD012991	Novel G p
35	14.2	52.6	38	6	BD014502	Novel G p
36	14.2	52.6	50	6	CQ007026	Sequence
37	14	51.9	42	6	BD231118	Shuffling
38	14	51.9	42	10	AB002263	Mus muscu
39	13.8	51.1	19	6	AR038723	Sequence
40	13.8	51.1	19	6	AR059609	Sequence
41	13.8	51.1	31	6	I92393	Sequence 45
42	13.8	51.1	31	6	I92395	Sequence 47
43	13.8	51.1	31	6	BD002902	Gene comp
44	13.8	51.1	48	6	CQ848125	Sequence
45	13.6	50.4	50	6	CQ008837	Sequence
46	13.6	50.4	20	6	AX319716	Sequence
47	13.6	50.4	33	6	AX468847	Sequence
48	13.6	50.4	41	6	AX514614	Sequence
49	13.6	50.4	41	6	AX520556	Sequence
50	13.4	49.6	23	6	A22727	oligonucleo
51	13.4	49.6	23	6	A47686	Sequence 4
52	13.4	49.6	23	6	I21369	Sequence 4
53	13.4	49.6	24	6	AX488576	Sequence
54	13.4	49.6	28	6	AR121174	Sequence
55	13.4	49.6	28	6	BD003589	Methods a
56	13.4	49.6	29	6	AR410189	Sequence
57	13.4	49.6	29	6	AX576982	Sequence
58	13.4	49.6	29	6	AX828555	Sequence
59	13.4	49.6	31	6	AR024399	Sequence
60	13.4	49.6	31	6	AR091772	Sequence
61	13.4	49.6	31	6	I71191	Sequence 43
62	13.4	49.6	31	6	I83750	Sequence 43
63	13.4	49.6	31	6	AR363050	Sequence
64	13.4	49.6	33	6	AR024400	Sequence
65	13.4	49.6	33	6	AR091773	Sequence
66	13.4	49.6	33	6	I71192	Sequence 44
67	13.4	49.6	33	6	I83751	Sequence 44
68	13.4	49.6	35	6	AX254702	Sequence
69	13.2	48.9	22	6	AX703202	Sequence
70	13.2	48.9	24	6	AX657568	Sequence
71	13.2	48.9	27	6	AR135179	Sequence
72	13.2	48.9	27	6	BD274686	Angiotens
73	13.2	48.9	27	6	AR382343	Sequence
74	13.2	48.9	27	6	AX418994	Sequence
75	13.2	48.9	28	6	CQ794114	Sequence
76	13.2	48.9	28	6	CQ800083	Sequence
77	13.2	48.9	29	6	BD140466	Secreted
78	13.2	48.9	30	6	BD143373	Oligonucl
79	13.2	48.9	33	6	BD179410	Screening
80	13.2	48.9	36	6	I03354	Sequence 4
81	13.2	48.9	42	6	AX060507	Sequence
82	13.2	48.9	42	6	AX317386	Sequence
83	13.2	48.9	45	6	AX317387	Sequence
84	13.2	48.9	45	6	AX283132	Sequence
85	13.2	48.9	49	6	AR075954	Sequence
86	13.2	48.9	49	6	AR322317	Sequence
87	13	48.1	23	6	AR067590	Sequence
88	13	48.1	26	6	BD143580	Method of
89	13	48.1	31	6	AX460476	Sequence
90	13	48.1	31	6	AX463680	Sequence
91	13	48.1	35	6	AX684693	Sequence
92	13	48.1	35	6	AX684695	Sequence